OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: March 2, 2005, 15:14:51 ; Search time 21 Seconds
               (without alignments)
               1828.118 Million cell updates/sec

Title: US-10-633-008-32
Perfect score: 2098
Sequence: 1 MGILGLILLGHITVDTYGR.........LLDTVPLDYEFLATEGKSVC 399

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :   PIR_79:*
               1: pir1:*
               2: pir2:*
               3: pir3:*
               4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score		Query Match Length	DB	ID	Description
1	178.5	8.5	299	2	S56749	junctional adhesio
2	178	8.5	7962	2	I38346	elastic titin - hu
3	170	8.1	365	2	JC7780	coxsackie- and ade
4	144.5	6.9	1033	2	S19247	cell adhesion prot
5	143.5	6.8	1052	2	B49120	protein-tyrosine k
6	139.5	6.6	3707	2	S18252	heparan sulfate pr
7	139	6.6	1106	1	PFHUGB	platelet-derived g
8	138.5	6.6	1323	2	PN0568	connectin/titin -
9	138.5	6.6	4162	2	T42633	connectin 3B - chi
10	138	6.5	584	2	T08678	connectin/titin -
11	136	6.5	5175	2	T20092	hypothetical prote
12	133.5	6.4	5198	2	T42290	hemicentin precurs
13	133.5	6.3	765	2	C42632	cell adhesion mole
14	132.5	6.3	812	2	B42632	cell adhesion mole
15	132.5	6.3	932	2	A42632	cell adhesion mole
16	132.5	6.3	1272	2	S26180	neurofascin - chic
17	132	6.3	1896	2	T08851	Down syndrome cell
18	131	6.3	4391	2	A38096	perlecan precursor
19	129.5	6.2	1040	2	A34695	axonal glycoprotei
20	129.5	6.2	3375	2	T19821	hypothetical prote
21	129.5	6.2	6658	2	T13931	projectin - fruit
22	129	6.1	309	2	I49922	gene B7-2 protein
23	129	6.1	1427	2	I51669	tumor suppressor -
24	129	6.1	1906	2	S68235	myosin-light-chain
25	128.5	6.1	338	2	JC5519	50K glycoprotein p
26	127	6.1	725	1	IJMSNG	neural cell adhesi
27	127	6.1	1115	1	IJMSNL	neural cell adhesi
28	125.5	6.0	1259	2	A43425	Bravo/Nr-CAM cell
29	125	6.0	351	2	JH0396	biliary glycoprote
30	124	5.9	853	1	IJBONC	neural cell adhesi
31	124	5.9	1011	2	T13669	neuromuscullin - fr
32	124	5.9	1344	2	T14316	rig-1 protein - mo
33	123.5	5.9	458	2	WMMSR1	biliary glycoprote
34	123.5	5.9	521	2	JC1508	biliary glycoprote
35	123.5	5.9	1091	1	IJCHNL	neural cell adhesi
36	123	5.9	464	1	C30127	transmembrane carc
37	123	5.8	467	1	HLMSP3	poliovirus recepto
38	123	5.8	526	2	A39640	biliary glycoprote
39	123	5.9	1694	2	JC2457	vascular cell adhe
40	122.5	5.8	538	2	A40096	platelet-endotheli
41	122.5	5.8	761	1	IJHUNG	neural cell adhesi
42	122.5	5.8	1268	2	S22383	biliary glycoprote
43	122	5.8	738	2	JC2457	sialoadhesin - mou
44	122	5.8	1036	2	A49151	axonin 1 precursor
45	121	5.8	816	2	JC1509	fibroblast growth
46	120.5	5.7	458	2	A31923	biliary glycoprote
47	120	5.7	333	2	JH0394	amalgam protein pr
48	119.5	5.7	417	2	T17346	biliary glycoprote
49	119.5	5.7	483	2	B45808	hypothetical prote
50	119.5	5.7	547	1	JE0100	B-lymphocyte antig
51	119.5	5.7	725	2	I48950	neural cell adhesi
52	119.5	5.7	917	1	TVHUP3	neural cell adhesi
53	119.5	5.7	806	2	A58532	telencephalin prec
54	119	5.7	1091	2	S68177	fibroblast growth
55	119	5.7	26926	1	S23969	titin, cardiac mus
56	119	5.6	547	2	A44783	glial cell membran
57	118.5	5.6	519	2	S28904	C-CAM2a protein is
58	118.5	5.6	1338	2	S09982	cell-adhesion mole
59	118	5.6	338	2	JC4776	ecto-ATPase precur
60	118	5.6	344	2	A27681	intercellular adhe
61	117.5	5.6	1092	1	JN0635	protein-tyrosine k
62	117.5	5.6	344	2	A32579	limbic-system-asso
63	117.5	5.6	1092	1	JS0675	nonspecific cross-
64	117.5	5.6	1239	1	IJRTNC	neural cell adhesi
65	117	5.6	739	2	A54100	neuroglian - fruit
66	117	5.6	858	1	I53960	vascular cell adhe
67	117	5.6	1447	2	A35963	neural cell adhesi
68	116.5	5.6	478	2	A49356	tumor suppressor p
69	116.5	5.6	806	2	A39712	PR2 alpha - human
70	116.5	5.6	1040	2	I55551	protein-tyrosine k
71	116.5	5.6	1051	2	S03421	transient axonal g
72	116	5.5	344	2	A40131	kinase-like protei
73	116	5.5	292	2	JB0099	neurotrimin - rat
74	115.5	5.5	293	2	A41060	T-cell receptor de
75	115.5	5.5	725	1	T42718	T-cell receptor de
76	115.5	5.5	1257	2	S34338	neural cell adhesi
77	115.5	5.5	1209	2	A53437	neural cell adhesi
78	115.5	5.5	602	2	I68093	probable neural ce
79	115	5.5	773	2	I61719	biliary glycoprote
80	114.5	5.5	417	1	IJXLNL	poliovirus recepto
81	114.5	5.4	1277	2	T25693	PR2 delta - human
82	114.5	5.4	321	2	S33766	neural cell adhesi
83	114.5	5.5	345	2	JC5018	biliary glycoprote
84	114.5	5.4	462	2	A45769	neural cell adhesi
85	114	5.4	518	2	QRRBG	acetylcholine rece
86	114	5.4	640	2	A44194	secretory componen
87	114	5.4	773	2	T30532	poliovirus recepto
88	113.5	5.4	1277	2	JH0395	neural cell adhesi
89	113	5.4	321	2	JC4025	biliary glycoprote
90	113	5.4	345	2	I38404	opioid-binding cel
91	112.5	5.4	462	2	JC4024	neu differentiatio
92	112.5	5.4	518	2	A43273	poliovirus recepto
93	112.5	5.4	640	2	S36126	heregulin precurso
94	112.5	5.4	1259	2	TDDFLK	neural cell adhesi
95	112.5	5.4	2029	2	A47299	protein-tyrosine-p
96	112.5	5.4	946	2	T29583	ror-related recept
97	112	5.3	976	2	T44405	hypothetical prote
98	112	5.3	1273	2	AH1393	sax-3 protein - Ca
99	112	5.3	1530	2	JC4593	peptidoglycan anch
100	111.5	5.3	1070	2	T29757	protein-tyrosine k
101	111.5	5.3	6642	2		protein UNC-89 - C
102	111	5.3				

No.	Score	%	Len	N	Accession	Description
103	110.5	5.3	349	2	A34815	carcinoembryonic a
104	110	5.2	417	2	RWHUPA	poliovirus recepto
105	110	5.2	626	1	BNRT3J	myelin-associated
106	110	5.2	1880	2	T16531	tractin - medicina
107	110	5.2	2295	2	C88369	protein unc-52 [im
108	109.5	5.2	338	2	JC1238	opioid-binding pro
109	109.5	5.2	345	2	JC1239	opioid-binding pro
110	109.5	5.2	526	2	S70587	butyrophilin precu
111	109.5	5.2	800	2	A48991	heparin-binding gr
112	109.5	5.2	801	2	S15363	fibroblast growth
113	109.5	5.2	1336	2	I60598	fibroblast growth
114	109	5.2	646	2	I38049	Flt-1 tyrosine kin
115	108.5	5.2	345	2	S03199	cell surface glyco
116	108.5	5.2	416	2	A54017	opioid-binding pro
117	108.5	5.2	637	2	B33785	colon carcinoma-as
118	108.5	5.2	819	1	TVCHFG	myelin-associated
119	108.5	5.2	1021	1	T42634	fibroblast growth
120	108.5	5.1	1328	2	T23007	connectin/titin -
121	108.5	5.1	526	2	A37821	hypothetical prote
122	108	5.1	636	1	I61718	butyrophilin - bov
123	108	5.1	1098	1	PFMSRB	neu differentiatio
124	108	5.1	1612	2	T30805	platelet-derived g
125	107.5	5.1	800	1	TVHU2F	duti protein - mo
126	107.5	5.1	818	2	JC4058	fibroblast growth
127	107.5	5.1	829	2	JC4583	fibroblast growth
128	107.5	5.1	354	1	S42938	proteoglycan link
129	106.5	5.1	662	2	C40862	heparin-binding gr
130	106.5	5.1	822	1	TVHUFG	fibroblast growth
131	106.5	5.1	1227	2	T23004	hypothetical prote
132	106.5	5.1	1232	2	T43027	neural cell adhesi
133	106.5	5.1	582	1	BNRT3S	myelin-associated
134	106	5.1	797	2	S38579	fibroblast growth
135	106	5.1	919	2	T32541	unc-5 protein - Ca
136	106	5.1	947	1	B44294	unc-5 protein, lon
137	106	5.1	1040	2	A57638	receptor tyrosine
138	106	5.0	1103	2	T22889	hypothetical prote
139	105.5	5.0	423	2	T29549	hypothetical prote
140	105.5	5.0	729	2	A56795	fibroblast growth
141	105.5	5.0	733	2	I49293	fibroblast growth
142	105.5	5.0	822	2	I49289	fibroblast growth
143	105.5	5.0	940	2	S29840	fibroblast growth
144	105.5	5.0	822	2	A40985	projectin - fruit
145	105.5	5.0	1256	2	T03096	CDO protein - rat
146	105	5.0	862	2	I49583	differentiation an
147	104.5	5.0	268	2	T23555	hypothetical prote
148	104.5	5.0	392	2	B44194	poliovirus recepto
149	104.5	5.0	599	2	T16774	hypothetical prote
150	104.5	5.0	1021	2	I39207	leukocyte surface
151	104.5	5.0	1184	2	T09484	cartilage intermed
152	104.5	5.0	2222	2	T13924	sdk protein - frui
153	104.5	5.0	2783	2	T34416	hypothetical prote
154	104	5.0	299	1	AHRB	B-cell adhesion pr
155	104	5.0	338	2	S09276	Ig alpha chain C r
156	104	5.0	637	2	C43273	heregulin precurso
157	104	5.0	662	2	I61722	neu differentiatio
158	104	5.0	882	2	I38912	receptor tyrosine
159	104	5.0	1356	2	JC1402	protein-tyrosine k
160	103.5	5.0	628	2	I38000	lutheran blood gro
161	103.5	5.0	647	2	A35648	B-cell adhesion pr
162	103.5	5.0	822	1	TVMSFG	fibroblast growth
163	103.5	5.0	824	2	S36439	fibroblast growth
164	103.5	5.0	832	2	JHO393	B-cell adhesion pr
165	103.5	5.0	847	2	JHO371	fibroblast growth
166	103.5	4.9	6831	2	A88852	protein unc-22 [im
167	103.5	4.9	6839	2	S57242	twitchin [similari
168	103.5	4.9	7160	2	T27935	hypothetical prote
169	103	4.9	811	2	A41054	fascicin II, tran
170	103	4.9	873	2	B41054	fascicin II PI-li
171	103	4.9	1742	2	S24600	projectin - fruit
172	103	4.9	318	2	F72171	KGR protein - vari
173	102.5	4.9	1176	2	JN0583	myosin-light-chain
174	102.5	4.9	1651	2	T14160	transmembrane rece
175	102.5	4.9	626	1	A61084	myelin-associated
176	102	4.9	702	2	A36319	carcinoembryonic a
177	102	4.9	871	2	I48696	protein-tyrosine k
178	102	4.9	881	1	I48697	protein-tyrosine k
179	101.5	4.9	392	1	RWHUPD	poliovirus recepto
180	101.5	4.8	413	2	S65948	hemolin precursor
181	101.5	4.8	413	2	A37778	hemolin - cecropia
182	101.5	4.8	898	2	A40114	fascicin II precu
183	101.5	4.8	1260	2	S05479	neural cell adhesi
184	101.5	4.8	1526	2	T13823	frazzled gene prot
185	101	4.8	267	2	T13442	probable tumor sup
186	101	4.8	288	2	T24824	hypothetical prote
187	101	4.8	355	1	LKCH	proteoglycan link
188	101	4.8	355	2	LKRT2	proteoglycan link
189	101	4.8	408	1	I50419	meprin A (BC 3.4.2
190	101	4.8	620	2	JH0593	s-glicerin precurso
191	101	4.8	584	2	I50128	Schwann cell myeli
192	101	4.8	713	2	A46512	fibroblast growth
193	101	4.8	868	2	A53743	fibroblast growth
194	100.5	4.8	890	1	T13822	hypothetical prote
195	100.5	4.8	1375	2	A48754	protein-tyrosine k
196	100.5	4.8	329	1	TVHUF4	fibroblast growth
197	100.5	4.8	329	2	A39627	fibroblast growth
198	100.5	4.7	354	2	A46254	CD4 precursor - ra
199	100	4.7	520	2	A44098	brain-derived neur
200	100	4.7	459	2	A31104	brain-derived neur
201	100	4.7	476	1	S06943	B7-2 antigen - hum
202	99.5	4.7	821	2	LKHU	proteoglycan link
203	99.5	4.7	812	1	A35104	brain-derived neur
204	99.5	4.7	1367	1	A36477	brain-derived neur
205	99.5	4.7	1379	1	I58164	BIG-1 protein - ra
206	99.5	4.7	1330	2	A41228	vascular endotheli
207	99.5	4.7	2025	2	S49010	skelemin - mouse
208	99.5	4.7	1666	2	I78875	hypothetical prote
209	99	4.7	1028	1	S12839	FP31 protein - fow
210	99	4.7	380	2	JC4166	31R protein - vari
211	99	4.7	313	2	A49120	pregnancy-specific
212	99	4.7	275	2	I37202	T-cell surface gly
213	99	4.7	424	2	I73631	heregulin, splice
214	99	4.7	458	2	I37702	hypothetical prote
215	99	4.7	645	2	A56853	fibroblast growth
216	99	4.7	773	1	I49152	brain-derived neur
217	98.5	4.7	812	2	AH1115	protein-tyrosine de
218	98.5	4.7	1028	2	I50600	embryonic receptor
219	98	4.7	1330	2	D24891	receptor tyrosine
220	98	4.7	1367	2	S55596	Ig heavy chain pre
221	98	4.7	880	2	OMHU1B	protein-tyrosine k
222	98	4.6	880	1	A41288	protein-tyrosine k
223	97.5	4.6	1499	2	T42597	T-cell receptor de
224	97.5	4.6	144	2	S24108	proteoglycan link
225	97.5	4.6	354	2	I42276	brain-derived neur
226	97.5	4.6	477	2	A53449	B-CAM protein - hu
227	97.5	4.6	588	2	A59307	fibroblast growth
228	97.5	4.6	764	2	S05050	irregular chiasm C
229	97.5	4.6	822	1	T00382	brain-derived neur
230	97.5	4.6	876	2	S46224	protein-tyrosine k
231	97.5	4.6	1348	2	A31326	cell surface prote
232	97.5	4.6	1443	2	T28598	neogenin - chicken
233	97	4.6	116	2	T13078	T-cell receptor al
234	97	4.6	307	2	T17404	hypothetical prote
235	97	4.6	474	2	A41288	alpha-1-B-glycopro
236	97	4.6	739	2	A42597	vascular cell adhe
237	97	4.6	751	2	S24108	DNA helicase/prima
238	97	4.6	824	2	I42276	protein-tyrosine k
239	97	4.6	994	2	A53449	c-mer protein-tyro
240	97	4.6	1028	2	A59307	myosin-light-chain
241	97	4.6	1147	2	S05050	plasmacytoma-assoc
242	97	4.6	1274	2	T00382	cardiac myosin-bin
243	97	4.6	1321	2	S46224	hypothetical prote
244	97	4.6	1535	2	A31326	peroxidasin - frui
245	96.5	4.6	288	2	T28598	T-cell receptor de
246	96.5	4.6	313	2	A31326	T-cell receptor de
247	96.5	4.6	772	2	T13078	hypothetical prote
248	96.5	4.6	1200	2	T17404	hyalin - sea urchi

No.	%		Length	n	Accession	Description
249	96.5	4.6	2013	2	AD1129	probable peptidogl
250	96	4.6	243	2	S25755	Ig lambda chain -
251	96	4.6	364	2	A30521	myeloid cell surfa
252	96	4.6	407	2	C82428	glucose-1-phosphat
253	96	4.6	739	2	JN0581	vascular cell adhe
254	96	4.6	1262	2	B48758	cell surface glyco
255	96	4.6	1483	2	C97012	protein-tyrosine-p
256	96	4.6	1496	2	A48758	probably cellulose
257	96	4.6	6805	2	S20901	titin - rabbit (fr
258	95.5	4.6	243	2	A52244	leukocyte antigen
259	95.5	4.6	328	2	S30444	ST2 protein - huma
260	95.5	4.6	887	2	AD2009	hypothetical prote
261	95.5	4.6	1132	2	A35089	myosin-binding pro
262	95	4.6	137	2	I46628	rearranged T-cell
263	95	4.5	814	1	A39752	fibroblast growth
264	95	4.5	1450	2	A44027	165K myofibrillar
265	95	4.5	1501	2	I58148	protein-tyrosine-p
266	95	4.5	1863	2	S46217	protein-tyrosine-p
267	95	4.5	1907	2	S50893	protein-tyrosine-p
268	95	4.5	1945	2	T13937	plexin A - fruit f
269	94.5	4.5	135	2	S36314	T-cell receptor de
270	94.5	4.5	315	1	HNV24X	hemagglutinin prec
271	94.5	4.5	588	2	JH0506	adhesion molecule
272	94.5	4.5	588	2	A45254	surface glycoprote
273	94.5	4.5	875	2	T33434	hypothetical prote
274	94.5	4.5	888	2	S23065	ufo protein - mous
275	94.5	4.5	999	2	I38547	novel cellular pro
276	94	4.5	118	2	I71934	MHC class II I-A-a
277	94	4.5	268	2	S45446	Ig heavy chain V r
278	94	4.5	313	2	H36854	hemagglutinin - va
279	94	4.5	422	2	S32357	glial growth facto
280	94	4.5	583	2	G84829	probable PTR2 fami
281	94	4.5	943	2	F69543	ATP-dependent RNA
282	94	4.5	1091	2	S01998	contactin precurso
283	94	4.5	1325	2	A64905	ydeK protein - Esc
284	94	4.5	1648	2	S61654	probable membrane
285	93.5	4.5	142	2	S36307	T-cell receptor de
286	93.5	4.5	259	2	JC7109	ST2V protein - hum
287	93.5	4.5	330	2	I46691	CD86 precursor - r
288	93.5	4.5	587	2	JH0464	DM-GRASP precursor
289	93.5	4.5	799	2	S18209	fibroblast growth
290	93.5	4.5	1038	2	T30304	protein RanBP7 - A
291	93.5	4.5	1240	2	T03097	CDO protein - huma
292	93	4.5	330	2	A29915	teratocarcinoma gl
293	93	4.5	432	1	RWC2T4	T-cell surface gly
294	93	4.5	435	2	D33258	pregnancy-specific
295	93	4.5	568	2	A45804	Ig mu chain C regi
296	93	4.5	625	2	T16777	hypothetical prote
297	93	4.5	1018	2	JC4211	neural adhesion pr
298	93	4.4	1094	2	S22573	DNA-directed DNA p
299	93	4.4	1643	2	T14274	versican precursor
300	93	4.4	3381	2	T42389	versican precursor
301	92.5	4.4	144	2	S36322	T-cell receptor de
302	92.5	4.4	275	2	JC7604	CD86 spliced varia
303	92.5	4.4	424	2	A34595	pregnancy-specific
304	92.5	4.4	474	1	C39667	brain-derived neur
305	92.5	4.4	476	1	B39667	brain-derived neur
306	92.5	4.4	764	1	QRHUGS	secretory componen
307	92.5	4.4	821	1	A39667	brain-derived neur
308	92	4.4	116	2	E24891	T-cell receptor al
309	92	4.4	132	2	A55410	Ig light chain V r
310	92	4.4	323	2	A48997	tumor surface anti
311	92	4.4	583	2	I39428	alcam - human
312	92	4.4	627	2	S14683	Ig mu chain precur
313	92	4.4	1005	2	I18537	Ig heavy chain - c
314	92	4.4	2482	2	I48922	cation-independent
315	92	4.4	2483	1	A49617	insulin-like growt
316	92	4.4	13055	2	T16580	hypothetical prote
317	91.5	4.4	240	2	JL0143	antigen BCM1 precu
318	91.5	4.4	576	2	A32604	hypothetical prote
319	91.5	4.4	647	2	B41288	interleukin 1 rece
320	91.5	4.4	1241	2	T37190	vascular cell adhe
321	91.5	4.4	1462	1	A69809	nephrin - human
322	91.5	4.4	2013	2	AI1489	probable peptidogl
323	91	4.3	282	2	T17219	hypothetical prote
324	91	4.3	789	2	T28714	hypothetical prote
325	91	4.3	829	1	IJHUCP	cadherin 3 precurs
326	91	4.3	1355	2	T28715	hypothetical prote
327	91	4.3	309	2	S15674	cell surface glyco
328	90.5	4.3	341	2	B95403	cell fusion glycop
329	90.5	4.3	361	2	PN0020	cell fusion glycop
330	90.5	4.3	449	2	A45557	hypothetical prote
331	90.5	4.3	452	1	MHHU	titin - mouse (fra
332	90.5	4.3	453	2	S37768	Ig mu chain C regi
333	90.5	4.3	473	2	MHHUM	Ig mu chain C regi
334	90.5	4.3	487	2	S65133	butyrophilin - mou
335	90.5	4.3	531	2	S20900	titin - mouse (fra
336	90.5	4.3	631	2	A48346	cell fusion glycop
337	90.5	4.3	631	2	VGN2PD	cell fusion glycop
338	90.5	4.3	860	2	JC5702	ErbB kinase activa
339	90.5	4.3	868	2	JC5701	ErbB kinase activa
340	90.5	4.3	526	2	T27581	hypothetical prote
341	90	4.3	682	2	A35969	calcium vector pro
342	90	4.3	821	1	TVHUF2	pregnancy-specific
343	90	4.3	453	2	A54744	pregnancy-specific
344	90	4.3	1018	2	E90893	protein-tyrosine k
345	90	4.3	1343	2	D85724	165K protein, skel
346	90	4.3	1343	2	B90893	protein-tyrosine k
347	89.5	4.3	142	2	S04664	chondroitin sulfat
348	89.5	4.3	157	2	S04915	proteoglycan link
349	89.5	4.3	243	2	A37980	rearranged T-cell
350	89.5	4.3	275	2	A37982	rearranged T-cell
351	89.5	4.3	335	2	A28928	T-cell receptor de
352	89.5	4.3	823	2	H43354	protein-tyrosine k
353	89.5	4.3	823	2	B35963	neuronal cell surf
354	89	4.2	1465	2	S43529	leukocyte common a
355	89	4.2	2325	2	A61208	colicin V secretio
356	89	4.2	101	2	A29165	neurolin - goldfis
357	89	4.2	145	2	I46629	fibroblast growth
358	89	4.2	279	2	S04693	fibroblast growth
359	89	4.2	282	2	C28928	keratinocyte growt
360	89	4.2	413	2	IKEC5A	fibroblast growth
361	89	4.2	523	2	I50478	peptidoglycan link
362	89	4.2	769	2	S16236	ErbB kinase activa
363	89	4.2	822	2	A45081	contactin precurso
364	89	4.2	822	2	A41794	hypothetical prote
365	89	4.2	822	2	S19947	chondroitin sulfat
366	89	4.2	941	2	B49151	190K protein - hum
367	89	4.2	1020	2	TVMVMD	myelin/oligodendro
368	89	4.2	1020	1	S05944	receptor tyrosine
369	88.5	4.2	1273	2	TDRTLT	activated B-cell p
370	88.5	4.2	2491	1	A28372	myelin/oligodendro
371	88.5	4.2	975	2	S35341	T-cell surface gly
372	88.5	4.2	3562	2	T42576	hypothetical prote
373	88	4.2	131	2	AB1283	kettin - fruit fly
374	88	4.2	247	2	A47171	insulin-like growt
375	88	4.2	344	1	F97302	secretory componen
376	88	4.2	691	1	QRRTGS	peptidoglycan link
377	88	4.2	769	1	JC5700	ErbB kinase activa
378	88	4.2	850	2	A57112	contactin precurso
379	88	4.2	1021	2	A29066	hypothetical prote
380	88	4.2	1043	2	P97302	chondroitin sulfat
381	88	4.2	1021	2	S42167	DNA ligase (ATP) (
382	88	4.2	1451	2	T30938	neural cell adhesi
383	87.5	4.2	2051	2	T30938	polymeric immunogl
384	87.5	4.2	205	2	A48929	alcohol dehydrogen
385	87.5	4.2	246	2	A47712	fasciclin III prec
386	87.5	4.2	474	2	S15590	myelin/oligodendro
387	87.5	4.2	508	2	A33378	Ig heavy chain - h
388	87.5	4.2	742	2	JS0326	activated B-cell p
389	87.5	4.2	757	2	I45056	receptor tyrosine
390	87.5	4.2	768	2	A29066	190K protein - hum
391	87.5	4.2	1197	2	T30581	hypothetical prote
392	87.5	4.2	1417	2	D85521	chondroitin sulfat
393	87.5	4.2	1493	2	T10757	contactin precurso
394	87.5	4.2	1897	1	TDHULK	leukocyte antigen-

No.	Score	E	Len	N	ID	Description
395	87	4.1	139	2	S36302	T-cell receptor de
396	87	4.1	365	2	I72171	HLA-Aw33.1, HLA-Aw
397	87	4.1	707	2	JC7763	neuronal leucine-r
398	87	4.1	818	2	T19120	hypothetical prote
399	87	4.1	936	2	I40711	sapB protein - Cam
400	87	4.1	1042	2	A97209	spoIID-like domain
401	87	4.1	1957	2	T38077	hypothetical coile
402	87	4.1	115	2	C24891	T-cell receptor al
403	86.5	4.1	310	1	HNVZRA	hemagglutinin prec
404	86.5	4.1	363	2	JH0542	class I histocompa
405	86.5	4.1	465	2	AB2211	MutT/nudix family
406	86.5	4.1	894	1	A41527	protein-tyrosine k
407	86.5	4.1	1348	2	B70969	vascular endotheli
408	86.5	4.1	3157	2	S51656	hypothetical prote
409	86.5	4.1	1894	2	S46689	protein-tyrosine k
410	86.5	4.1	1637	2	T46438	probable PPE prote
411	86.5	4.1	1363	2	I58375	T-cell receptor al
412	86.5	4.1	116	2	B24891	rearranged T-cell
413	86	4.1	150	2	I46624	alpha-agglutinin (
414	86	4.1	270	2	A34636	Fc-gamma receptor
415	86	4.1	357	2	S09265	Ig alpha chain C r
416	86	4.1	398	2	S17428	interleukin-1 rece
417	86	4.1	421	2	T46266	hypothetical prote
418	86	4.1	480	2	B56182	fibroblast growth
419	86	4.1	497	2	JC2456	pyruvate kinase (E
420	86	4.1	650	2	S22835	alpha-agglutinin -
421	86	4.1	964	2	T15746	hypothetical prote
422	86	4.1	975	1	TVMSKT	protein-tyrosine k
423	86	4.1	980	1	TVCTMD	macrophage colony-
424	86	4.1	1241	2	H84486	probable helicase
425	86	4.1	1327	2	T09402	immunoglobulin-lik
426	86	4.1	1345	2	H90975	hypothetical prote
427	86	4.1	2660	2	E85822	probable invasin Z
428	85.5	4.1	210	2	A56169	Ig kappa chain V r
429	85.5	4.1	216	2	JE0045	Ig lambda chain NI
430	85.5	4.1	218	2	S68241	Ig kappa chain V r
431	85.5	4.1	302	2	A86983	conserved hypothet
432	85.5	4.1	329	2	S72760	ppsl protein - Myc
433	85.5	4.1	329	2	A44065	hypothetical prote
434	85.5	4.1	332	2	C83610	fibroblast growth
435	85.5	4.1	388	2	B48899	beta-lactamase (EC
436	85.5	4.1	397	2	C43354	sulfate-binding pr
437	85.5	4.1	419	2	JC4123	pregnancy-specific
438	85.5	4.1	869	2	T19226	conserved hypothet
439	85.5	4.1	869	2	C88364	protein C13B4.1 [1
440	85.5	4.1	1002	2	S37928	probable purine nu
441	85.5	4.1	1028	2	D54689	protein-tyrosine-p
442	85.5	4.1	1518	2	T29340	hypothetical prote
443	85.5	4.1	1691	2	S07705	T-cell receptor al
444	85.5	4.1	2541	2	S36303	T-cell receptor de
445	85.5	4.1	104	2	A33402	pregnancy-specific
446	85.5	4.1	137	2	S58394	myelin/oligodendro
447	85.5	4.1	166	2	A55811	carcinoembryonic a
448	85.5	4.1	247	2	B28928	pregnancy-specific
449	85	4.1	265	2	G43354	pregnancy-specific
450	85	4.1	273	2	F43354	pregnancy-specific
451	85	4.1	324	2	A43354	pregnancy-specific
452	85	4.1	326	2	I57486	pregnancy-specific
453	85	4.1	333	2	JS0032	pregnancy-specific
454	85	4.1	428	2	A56182	fibroblast growth
455	85	4.1	428	2	PQ0666	envelope protein -
456	85	4.1	480	2	TS1246	ARR1 protein [impo
457	85	4.1	496	2	S41628	genome polyprotein
458	85	4.1	669	2	S51592	XynB precursor - R
459	85	4.1	776	2	TVMSBK	fibroblast growth
460	85	4.1	781	1	A47543	homolog of Drosoph
461	85	4.1	821	2	I38757	R-cadherin precurs
462	85	4.1	904	1	I38756	homolog of Drosoph
463	85	4.1	913	2	A42265	alpha-mannosidase
464	85	4.1	926	1	S60613	protein-tyrosine-p
465	85	4.1	1005	2	A60979	versican precursor
466	85	4.1	1216	2	T13719	versican precursor
467	85	4.1	2409/4116	1/2	—	calo protein - fru

No.	Score	E	Len	N	ID	Description
468	84.5	4.0	241	2	S32259	glial growth facto
469	84.5	4.0	264	2	P27579	T-cell receptor al
470	84.5	4.0	266	2	T29613	hypothetical prote
471	84.5	4.0	286	2	A28833	carcinoembryonic a
472	84.5	4.0	419	2	A33258	pregnancy-specific
473	84.5	4.0	419	2	A31135	pregnancy-specific
474	84.5	4.0	432	2	S30193	T-cell surface gly
475	84.5	4.0	436	2	S30371	T-cell surface gly
476	84.5	4.0	457	2	B69371	bile acid-inducibl
477	84.5	4.0	457	2	A27449	T-cell surface gly
478	84.5	4.0	568	2	AI1476	gene DMR-N9 protei
479	84.5	4.0	642	2	S36845	oligopeptide ABC t
480	84.5	4.0	795	2	I58106	hypothetical prote
481	84.5	4.0	874	2	B72215	myosin-binding pro
482	84.5	4.0	1142	2	E97302	hypothetical prote
483	84.5	4.0	1349	2	T30261	chitinase (EC 3.2.
484	84.5	4.0	1433	2	S61441	surface-associated
485	84	4.0	2508	2	C90909	probable major tai
486	84	4.0	238	2	JC7593	SH2 domain-contain
487	84	4.0	255	2	HNV2VT	hemagglutinin - va
488	84	4.0	315	1	T37438	hemagglutinin prec
489	84	4.0	315	2	JL0118	Fc gamma (IgG) rec
490	84	4.0	317	2	D39371	Ig V-region-like B
491	84	4.0	321	2	S42632	Fit-1S protein pre
492	84	4.0	336	2	I51174	Ig heavy chain - R
493	84	4.0	381	2	T09062	probable advanced
494	84	4.0	402	2	E43354	pregnancy-specific
495	84	4.0	406	2	B43354	pregnancy-specific
496	84	4.0	473	2	T35997	conserved hypothet
497	84	4.0	621	2	B57431	myosin-binding C-p
498	84	4.0	705	2	S51635	fibroblast growth
499	84	4.0	707	2	A38429	keratinocyte growt
500	84	4.0	939	2	AF2503	hypothetical prote
501	84	4.0	977	2	I45877	protein-tyrosine k
502	84	4.0	987	2	A88746	protein C18F3.2 [i
503	84	4.0	1065	2	H95321	NolG efflux transp
504	84	4.0	1287	2	T30988	hypothetical prote
505	84	4.0	1912	2	A56178	protein-tyrosine-p
506	83.5	4.0	2397	1	A55535	versican precursor
507	83.5	4.0	275	2	RWHUAC	T-cell receptor al
508	83.5	4.0	288	2	A45803	B-cell-restricted
509	83.5	4.0	329	2	AG0010	exported sulfate-b
510	83.5	4.0	339	2	S09264	fibroblast growth
511	83.5	4.0	363	2	S07113	Ig alpha chain C r
512	83.5	4.0	372	2	C39371	class I histocompa
513	83.5	4.0	496	2	S60685	Ig V-region-like B
514	83.5	4.0	498	2	S11246	envelope protein B
515	83.5	4.0	527	2	D75127	LAG-3 protein prec
516	83.5	4.0	590	2	I56526	hypothetical prote
517	83.5	4.0	629	2	AE1525	interleukin 1 rece
518	83.5	4.0	748	2	S41050	hypothetical prote
519	83.5	4.0	750	2	S41051	probable peptidogl
520	83.5	4.0	911	2	I56552	fibroblast growth
521	83.5	4.0	916	2	T05360	synapse-associated
522	83.5	4.0	976	1	TVHUKT	probable potassium
523	83.5	4.0	1032	2	T34433	protein-tyrosine k
524	83.5	4.0	2163	2	T15276	class I histocompa
525	83.5	4.0	2232	2	T34434	Ig V-region-like B
526	83.5	4.0	3898	1	GNWVHC	hypothetical prote
527	83	4.0	115	2	B32071	genome polyprotein
528	83	4.0	233	2	S25747	T-cell receptor de
529	83	4.0	416	2	G83656	Ig lambda chain -
530	83	4.0	422	2	B95001	hypothetical prote
531	83	4.0	428	2	A27658	conserved domain p
532	83	4.0	445	2	A97873	pregnancy-specific
533	83	4.0	977	2	S49004	conserved hypothet
534	83	4.0	1151	2	A45226	tyrosine kinase Mp
535	83	4.0	1188	2	A57064	integrin alpha-1 c
536	83	4.0	1211	1	S68251	hypothetical prote
537	82.5	4.0	2302	2	T14328	protein-tyrosine-p
538	82.5	3.9	3029	2	S76109	phospholipase C, i
539	82.5	3.9	185	2	S37479	T-cell receptor al
540	82.5	3.9	218	2	JC5810	hypothetical prote
	82.5	3.9	218	2	B47712	monoclonal antibod
	82	3.9	218	2		myelin/oligodendro

Seq	Score		Length		Accession	Description
541	82.5	3.9	229	2	A46527	B-cell-specific me
542	82.5	3.9	230	2	A56210	neu differentiatio
543	82.5	3.9	304	2	F87701	histone deacetylas
544	82.5	3.9	316	2	C37028	MHC class I histoc
545	82.5	3.9	353	2	S51242	heparin-binding fi
546	82.5	3.9	355	2	I80169	class I histocompa
547	82.5	3.9	356	1	S55437	translation releas
548	82.5	3.9	395	2	D43354	pregnancy-specific
549	82.5	3.9	417	2	A28277	pregnancy-specific
550	82.5	3.9	453	2	B83380	hypothetical prote
551	82.5	3.9	509	2	JC5288	SHP substrate-1 pr
552	82.5	3.9	513	2	JC5289	SHP substrate-1 pr
553	82.5	3.9	640	2	B84478	probable replicati
554	82.5	3.9	651	2	A96781	unknown protein F9
555	82.5	3.9	666	2	D82511	1,4-alpha-glucan b
556	82.5	3.9	757	1	S48841	secretory componen
557	82.5	3.9	793	2	S59067	penton long fiber
558	82.5	3.9	942	2	S23251	protein-tyrosine k
559	82.5	3.9	1015	2	T32186	hypothetical prote
560	82	3.9	147	2	I46625	rearranged T-cell
561	82	3.9	150	2	S36312	T-cell receptor de
562	82	3.9	230	2	S26199	plastoquinol-plast
563	82	3.9	242	2	S06942	hypothetical prote
564	82	3.9	250	2	H81854	probable zinc-bind
565	82	3.9	261	2	C85681	hypothetical prote
566	82	3.9	335	2	A33514	pregnancy-specific
567	82	3.9	340	2	T28137	Ig alpha chain r
568	82	3.9	352	2	S02266	pregnancy-specific
569	82	3.9	374	2	F69233	carbamoyl-phosphat
570	82	3.9	426	2	C55181	pregnancy-specific
571	82	3.9	426	2	S09016	pregnancy-specific
572	82	3.9	426	2	B55334	pregnancy-specific
573	82	3.9	436	2	B55181	pregnancy-specific
574	82	3.9	684	2	P91148	aldehyde:ferredoxi
575	82	3.9	704	2	T31227	tran protein homol
576	82	3.9	707	2	A54846	fibroblast growth
577	82	3.9	822	2	B54846	fibroblast growth
578	82	3.9	1086	2	AF1662	cellobiose-phospho
579	82	3.9	1160	2	F88369	protein unc-52 [im
580	82	3.9	1198	2	T49726	hypothetical prote
581	82	3.9	1378	1	I48751	protein-tyrosine k
582	82	3.9	1385	2	D89824	hypothetical prote
583	82	3.9	1778	2	AF1116	internalin protein
584	82	3.9	1832	2	T31113	hypothetical prote
585	82	3.9	1898	2	S46216	leukocyte antigen-
586	82	3.9	4006	2	T09070	probable tenascin
587	81.5	3.9	85	2	S0809	carcinoembryonic a
588	81.5	3.9	140	2	C24747	T-cell receptor be
589	81.5	3.9	213	2	S66213	Ig heavy chain (Ma
590	81.5	3.9	235	2	IS0610	T-cell surface gly
591	81.5	3.9	283	1	FCMSG1	Fc gamma (IgG) rec
592	81.5	3.9	314	1	HNV2VW	hemagglutinin prec
593	81.5	3.9	339	2	JQ1793	hemagglutinin prec
594	81.5	3.9	339	2	T28138	Ig V-region-like B
595	81.5	3.9	426	2	A35964	pregnancy-specific
596	81.5	3.9	650	1	JC1450	fibroblast growth
597	81.5	3.9	687	2	A49636	soluble vascular e
598	81.5	3.9	699	2	AI2686	proteinase II [imp
599	81.5	3.9	699	2	E97468	dipeptidyl aminope
600	81.5	3.9	1015	2	T32284	hypothetical prote
601	81.5	3.9	3507	2	T34513	hypothetical prote
602	81	3.9	117	2	S49983	T-cell receptor alp
603	81	3.9	139	2	I46630	rearranged T-cell
604	81	3.9	145	2	I46631	rearranged T-cell
605	81	3.9	206	2	A40305	biliary glycoprote
606	81	3.9	315	1	HNV2VW	hemagglutinin prec
607	81	3.9	432	1	RWMQT4	T-cell surface gly
608	81	3.9	438	2	E96545	hemagglutinin prec
609	81	3.9	450	2	S25162	hypothetical prote
610	81	3.9	509	2	JC6203	gag protein - feli
611	81	3.9	645	2	T49702	SP8 binding protei
612	81	3.9	673	2	S46520	related to DOSI pr
613	81	3.9	767	2	F86383	luciferin-binding

Seq	Score		Length		Accession	Description
614	81	3.9	823	2	S48873	zC21.2 protein - C
615	81	3.9	846	1	T19179	hypothetical prote
616	81	3.9	978	1	A49814	protein-tyrosine k
617	81	3.9	990	2	T16554	MHC class I histoc
618	81	3.9	1001	2	T00532	probable cadmium-t
619	81	3.9	1172	2	F84572	probable cadmium-t
620	81	3.9	1433	1	A36734	bacillopeptidase F
621	81	3.9	1492	2	T14652	protein J's, Yersin
622	81	3.9	1545	2	T14966	phage lambda-relat
623	81	3.9	1650	2	S53457	dominant autoantig
624	81	3.9	1806	2	AF1717	probable peptidogl
625	81	3.9	3488	2	T34418	hypothetical prote
626	81	3.9	133	2	S57870	T cell receptor Ck
627	80.5	3.8	142	2	B28344	VpreB protein prec
628	80.5	3.8	366	2	I37523	MHC class I histoc
629	80.5	3.8	426	2	B33258	pregnancy-specific
630	80.5	3.8	426	2	A35341	pregnancy-specific
631	80.5	3.8	441	2	T31482	hypothetical prote
632	80.5	3.8	551	2	A30342	interleukin-2 rece
633	80.5	3.8	698	2	D81832	transferrin-bindin
634	80.5	3.8	820	2	S17295	fibroblast growth
635	80.5	3.8	874	2	T29548	hypothetical prote
636	80.5	3.8	878	1	A83748	endo-beta-N-acetyl
637	80.5	3.8	960	2	JN0677	protein-tyrosine k
638	80.5	3.8	1507	2	D97106	large chain of NAD
639	80.5	3.8	1641	2	D82704	conserved hypothet
640	80.5	3.8	1124	1	P83560	probable type II s
641	80.5	3.8	133	2	I46632	rearranged T-cell
642	80	3.8	147	2	T29925	T-cell receptor al
643	80	3.8	194	1	A36040	Ig heavy chain V-I
644	80	3.8	218	2	S71192	hypothetical prote
645	80	3.8	287	2	A37284	surface-array prot
646	80	3.8	304	1	RWCHH7	probable secreted
647	80	3.8	309	2	I49503	cell surface glyco
648	80	3.8	365	2	A45847	B-lymphocyte activ
649	80	3.8	403	2	AB0640	myosin-binding pro
650	80	3.8	403	2	S10365	hypothetical prote
651	80	3.8	549	1	S04845	Ca2+-transporting
652	80	3.8	559	1	S55383	hypothetical prote
653	80	3.8	701	2	T17243	hypothetical prote
654	80	3.8	748	2	T37097	probable secreted
655	80	3.8	893	2	A37284	surface-array prot
656	80	3.8	939	2	AE2275	hypothetical prote
657	80	3.8	999	2	S72267	hypothetical prote
658	80	3.8	1123	2	S36846	flagellar hook pro
659	80	3.8	1582	2	T15308	flagellar hook pre
660	80	3.8	2481	2	A43908	flagellar hook pro
661	80	3.8	2824	1	T22759	fibronectin - Afri
662	79.5	3.8	104	2	J36305	hypothetical prote
663	79.5	3.8	114	2	JH0341	hypothetical prote
664	79.5	3.8	135	2	S36298	MHC Ch1A chain - c
665	79.5	3.8	137	2	C45093	B7 protein - human
666	79.5	3.8	137	2	C70748	fibroblast growth
667	79.5	3.8	140	1	I46638	Ig lambda chain -
668	79.5	3.8	147	2	I46623	rearranged T-cell
669	79.5	3.8	232	2	S25756	rearranged T-cell
670	79.5	3.8	254	2	C42691	hypothetical prote
671	79.5	3.8	289	2	G00031	T-cell receptor de
672	79.5	3.8	313	2	I36958	T-cell receptor al
673	79.5	3.8	335	2	S09275	T-cell receptor al
674	79.5	3.8	341	2	S16521	T-cell receptor de
675	79.5	3.8	360	2	S09271	mitosis-specific c
676	79.5	3.8	361	2	S68089	Ig alpha chain C r
677	79.5	3.8	389	1	F64426	Ig alpha chain C r
678	79.5	3.8	474	2	B82227	actin 2 - Arabidop
679	79.5	3.8	481	2	S62427	phosphate-binding
680	79.5	3.8	483	1	B82227	exodeoxyribonuclea
681	79.5	3.8	495	2	A97744	G-protein signalin
682	79.5	3.8	531	2	A55181	isocitrate dehydro
683	79.5	3.8	570	2	JT0531	pregnancy-specific
684	79.5	3.8	637	2	T47673	muscarinic acetylc
685	79.5	3.8	610	2	A55939	peptide transport-
685	79.5	3.8	570	2	T49099	dihydrolipoamide S
686	79.5	3.8	924	2	S34926	dihydrolipoamide S
						hypothetical prote

Left block

No.	Score	Val	Len	N	Accession	Description
687	79.5	3.8	974	2	S34189	starch phosphoryla
688	79.5	3.8	1209	2	T14357	homeodomain-intera
689	79.5	3.8	1251	2	T21189	hypothetical prote
690	79.5	3.8	1265	1	A37967	neural cell adhesi
691	79.5	3.8	1663	2	C3RT	complement C3 prec
692	79.5	3.8	2218	1	B84883	hypothetical prote
693	79.5	3.8	3600	2	D86161	F1003.12 protein -
694	79	3.8	118	2	S04519	Ig lambda chain -
695	79	3.8	132	2	PQ0060	T-cell receptor be
696	79	3.8	210	2	JC4122	pregnancy-specific
697	79	3.8	226	2	S25745	Ig lambda chain -
698	79	3.8	241	2	D43273	heregulin precurso
699	79	3.8	345	2	A46052	vascular cell adhe
700	79	3.8	370	2	S29339	aggrecan - pig (fr
701	79	3.8	374	2	A46352	ORF1 protein - Chl
702	79	3.8	407	2	T08732	hypothetical prote
703	79	3.8	451	2	S71754	cellular hepatitis
704	79	3.8	502	2	T02746	cyclin A-like prot
705	79	3.8	567	2	S29498	lymphocyte antigen
706	79	3.8	716	1	WZBEE6	77.8K DNA helicase
707	79	3.8	741	2	E83265	probable two-compo
708	79	3.8	742	2	F84643	hypothetical prote
709	79	3.8	1250	2	E81339	probable restricti
710	79	3.8	1255	2	T06267	nematodes resistan
711	79	3.8	1298	2	A46999	protein-tyrosine k
712	79	3.8	1315	2	T28679	fibrinogen-binding
713	79	3.8	1388	2	T38720	chromodomain helic
714	79	3.8	3414	1	GNWVNE	genome polyprotein
715	78.5	3.7	136	2	JQ0473	class I histocompa
716	78.5	3.7	136	2	S36320	MHC class I histoc
717	78.5	3.7	215	2	A57843	sodium channel bet
718	78.5	3.7	230	2	S33161	Ig kappa chain - s
719	78.5	3.7	250	2	S11915	2',3'-cyclic-nucle
720	78.5	3.7	269	2	S57494	conserved hypothet
721	78.5	3.7	270	2	S65739	pregnancy-specific
722	78.5	3.7	279	2	S53363	hypothetical prote
723	78.5	3.7	324	2	S36646	basigin precursor
724	78.5	3.7	335	2	A75563	mucin 5AC (clone J
725	78.5	3.7	355	2	I80171	integrin-associate
726	78.5	3.7	363	2	S03537	inositol monophosp
727	78.5	3.7	366	2	I37544	class I histocompa
728	78.5	3.7	366	2	S42823	MHC class I histoc
729	78.5	3.7	366	2	B37028	MHC class I histoc
730	78.5	3.7	407	2	C83589	conserved hypothet
731	78.5	3.7	419	2	B54312	pregnancy-specific
732	78.5	3.7	484	2	B64481	hypothetical prote
733	78.5	3.7	568	2	A34891	Ig heavy chain pre
734	78.5	3.7	592	2	S25345	Ig mu chain pre
735	78.5	3.7	600	2	S25705	inner membrane cop
736	78.5	3.7	612	2	A82043	E-selection precurs
737	78.5	3.7	787	2	B42755	probable lipoprote
738	78.5	3.7	916	2	S73873	cadherin 4 precurs
739	78.5	3.7	1059	2	C38992	hypothetical prote
740	78.5	3.7	1243	2	T22545	sex factor aggrega
741	78.5	3.7	1609	2	S60138	hyperplastic discs
742	78	3.7	2895	2	T08437	probable membrane
743	78	3.7	95	2	B98068	hypothetical prote
744	78	3.7	121	2	A29080	T-cell receptor al
745	78	3.7	335	2	C54312	pregnancy-specific
746	78	3.7	342	2	E71101	probable geranylge
747	78	3.7	367	2	AB3303	probable putrescine-binding
748	78	3.7	519	2	JC4626	6-phosphofructo-2-
749	78	3.7	555	2	D71444	probable thioester
750	78	3.7	607	2	A95122	yacH protein - Esc
751	78	3.7	617	2	E64734	novel antigen rece
752	78	3.7	684	2	S60266	killer cell inhibi
753	78	3.7	841	2	S05894	Tn5252, relaxase [
754	78	3.7	886	2	JC5894	probable serine/th
755	78	3.7	941	2	S29605	glycoprotein 350/2
756	78	3.7	1185	2	T49136	protein kinase-lik
757	78	3.7	1203	2	A42404	collagen adhesin -
758	78	3.7	1335	2	T04294	xanthine dehydroge
759	78	3.7	3848	2	S07245	TipC protein - sli

Right block

No.	Score	Val	Len	N	Accession	Description
760	77.5	3.7	103	2	S36057	Ig lambda chain -
761	77.5	3.7	104	2	G24402	T-cell receptor al
762	77.5	3.7	122	2	S16439	Ig lambda chain -
763	77.5	3.7	134	2	A45693	T-cell receptor al
764	77.5	3.7	182	2	I83053	pregnancy-specific
765	77.5	3.7	227	2	A33937	Ig light chain (13
766	77.5	3.7	235	2	S25758	Ig lambda chain -
767	77.5	3.7	240	2	JC4121	pregnancy-specific
768	77.5	3.7	288	2	S29690	Ig heavy chain VDJ
769	77.5	3.7	295	2	A37412	pregnancy-specific
770	77.5	3.7	324	2	T18790	hypothetical prote
771	77.5	3.7	332	2	JN0067	MHC class I histoc
772	77.5	3.7	363	2	S42102	pregnancy-specific
773	77.5	3.7	364	2	S59931	glycerophosphodies
774	77.5	3.7	364	2	S59932	glycerophosphodies
775	77.5	3.7	364	2	S59933	glycerophosphodies
776	77.5	3.7	364	2	A43576	glycerophosphodies
777	77.5	3.7	364	2	S59934	glycerophosphodies
778	77.5	3.7	400	2	A39822	leukosialin precur
779	77.5	3.7	420	1	H84182	hypothetical precur
780	77.5	3.7	468	1	B84540	acid phosphatase (
781	77.5	3.7	496	2	S60686	envelope protein E
782	77.5	3.7	509	2	S17597	Ig delta chain (WI
783	77.5	3.7	537	2	A46611	myosin-binding pro
784	77.5	3.7	542	2	S49219	fiber protein - ca
785	77.5	3.7	557	2	H69678	meprin A (EC 3.4.2
786	77.5	3.7	594	2	T50013	hypothetical prote
787	77.5	3.7	662	2	T16525	involved in polyke
788	77.5	3.7	704	2	A48040	hypothetical prote
789	77.5	3.7	1005	2	C71513	hypothetical prote
790	77.5	3.7	1009	2	S26512	CryIAc toxin-bindi
791	77.5	3.7	1015	2	B87992	protein W09G3.1a l
792	77.5	3.7	1022	2	T48358	hypothetical prote
793	77.5	3.7	1036	2	B69368	hypothetical prote
794	77.5	3.7	1047	2	T41343	hypothetical prote
795	77.5	3.7	1141	2	E89824	probable translati
796	77.5	3.7	1156	2	T31517	hypothetical prote
797	77.5	3.7	1626	2	T23308	rifin [PFB0060w - m
798	77.5	3.7	1997	1	T26318	hypothetical prote
799	77.5	3.7	2470	1	S12050	protein-tyrosine-p
800	77	3.7	95	2	D95201	cation-independent
801	77	3.7	113	2	JH0340	hypothetical prote
802	77	3.7	135	2	S36323	T-cell receptor al
803	77	3.7	146	2	T15747	T-cell receptor de
804	77	3.7	309	2	E83687	hypothetical prote
805	77	3.7	329	2	T38444	T-cell receptor al
806	77	3.7	331	2	F71624	hypothetical prote
807	77	3.7	356	2	T51281	tapasin 1 homolog,
808	77	3.7	367	1	MHCH	Internalin A [Limo
809	77	3.7	396	2	T20772	type II transposas
810	77	3.7	403	2	T45033	dipeptidyl-peptida
811	77	3.7	430	2	I52590	hypothetical prote
812	77	3.7	433	2	T28143	envelope glycoprot
813	77	3.7	462	2	T17289	MHCH
814	77	3.7	463	2	A41158	hypothetical prote
815	77	3.7	496	2	A42707	m33-B isoform - mo
816	77	3.7	630	2	A43383	hypothetical prote
817	77	3.7	639	2	B54078	killer cell inhibi
818	77	3.7	661	2	JC5895	methyl-accepting c
819	77	3.7	680	2	B84638	hypothetical prote
820	77	3.7	690	2	AB1129	beta-D-glucan exoh
821	77	3.7	800	1	A42707	Ig mu chain C regi
822	77	3.7	840	2	S38001	hypothetical prote
823	77	3.7	928	1	A42707	hypothetical prote
824	77	3.6	1143	2	A57036	SNF2 protein homol
825	77	3.6	1156	1	S46122	phytochrome B - so
826	77	3.6	1666	2	T07756	clathrin heavy cha
827	77	3.6	2491	2	T33393	talin - slime mold
828	77	3.6	114	2	A57036	T-cell receptor be
829	77	3.6	115	2	I38116	T-cell receptor de
830	77	3.6	120	2	S03513	rearranged T-cell
831	77	3.6	151	2	I46626	T-cell receptor de
832	76.5	3.6	229	2	H86874	50S ribosomal prot

No.	%	%	Len	n	Accession	Description
833	76.5	3.6	239	2	G97165	flagellar hook ass
834	76.5	3.6	240	2	S01299	OX-45 membrane gly
835	76.5	3.6	240	2	A39016	T-cell surface gly
836	76.5	3.6	255	2	JQ1240	hypothetical 29.3K
837	76.5	3.6	296	2	B39581	GRSAG protein 9u
838	76.5	3.6	299	2	I46690	CD80 precursor - r
839	76.5	3.6	318	2	H75157	daunorubicin resis
840	76.5	3.6	330	2	A40071	Fc gamma (IgG) rec
841	76.5	3.6	336	2	I48471	Fc gamma (IgG) rec
842	76.5	3.6	404	2	A46480	Fc gamma (IgG).rec
843	76.5	3.6	451	2	T30603	perlecan homolog 2
844	76.5	3.6	477	2	H75026	oligopeptide abc t
845	76.5	3.6	501	2	A42030	alpha-globin trans
846	76.5	3.6	503	2	JC5287	SHP substrate-1 pr
847	76.5	3.6	530	2	T18896	hypothetical prote
848	76.5	3.6	599	2	T15552	hypothetical prote
849	76.5	3.6	632	2	H83106	chemotactic transd
850	76.5	3.6	742	2	S38093	probable purine nu
851	76.5	3.6	771	2	A83348	probable aldehyde
852	76.5	3.6	838	2	I45557	eyeless, long form
853	76.5	3.6	868	2	D86349	hypothetical prote
854	76.5	3.6	874	2	C84513	Mutator-like trans
855	76.5	3.6	886	2	T10890	hypothetical prote
856	76.5	3.6	980	2	T49570	cysteine proteinas
857	76.5	3.6	1110	2	T19673	hypothetical prote
858	76.5	3.6	1131	2	T09701	phytochrome - Scot
859	76.5	3.6	1138	2	S24614	myosin-binding pro
860	76.5	3.6	1311	2	T37757	hypothetical prote
861	76.5	3.6	1350	2	AF2005	RNA polymerase bet
862	76.5	3.6	1355	2	T30198	alkaline phosphata
863	76.5	3.6	2201	2	AH0095	probable sidero pho
864	76	3.6	120	1	P24402	T-cell receptor de
865	76	3.6	133	2	C26945	Ig lambda chain -
866	76	3.6	141	2	S36318	T-cell receptor de
867	76	3.6	145	2	S25743	T-cell receptor al
868	76	3.6	149	2	S36317	Fc gamma (IgG) rec
869	76	3.6	323	2	S06946	cAMP response elem
870	76	3.6	341	2	S26686	MHC class I histoc
871	76	3.6	360	2	A27638	HLA-B*5602 - human
872	76	3.6	362	2	I72755	HLA-B*5601 - human
873	76	3.6	362	2	I77754	MHC class I histoc
874	76	3.6	365	2	I38439	lymphocyte antigen
875	76	3.6	366	2	I81231	Ig mu heavy chain
876	76	3.6	391	1	I39131	probable acyl-CoA
877	76	3.6	400	2	AD3364	branched-chain ami
878	76	3.6	401	2	AG3552	alpha-methylacyl-C
879	76	3.6	415	2	AB3637	hypothetical prote
880	76	3.6	441	2	H96817	probable uridylyl
881	76	3.6	443	2	A96818	T-cell surface gly
882	76	3.6	446	2	F84451	chitinase and chit
883	76	3.6	457	1	RWMST4	protein E - Tick-b
884	76	3.6	478	2	AF1758	hypothetical prote
885	76	3.6	496	2	PC4408	protein containing
886	76	3.6	507	2	S52348	halolysin R4 (EC 3
887	76	3.6	511	2	A97212	hypothetical prote
888	76	3.6	519	2	S71451	hypothetical prote
889	76	3.6	555	2	T01142	hypothetical 63.2K
890	76	3.6	562	2	A65166	probable enzyme [i
891	76	3.6	562	2	B91194	probable enzyme yi
892	76	3.6	562	2	C86041	hypothetical prote
893	76	3.6	609	2	T16135	hypothetical prote
894	76	3.6	649	2	T32755	internalin A precu
895	76	3.6	723	2	S40127	probable coat prot
896	76	3.6	800	2	S37387	hypothetical prote
897	76	3.6	871	2	T46692	receptor-like prot
898	76	3.6	959	1	T45692	outer capsid prote
899	76	3.6	1245	2	P2XR13	related to multifu
900	76	3.6	1497	2	T49815	procollagen type V
901	76	3.6	1537	2	JC4172	DNA (cytosine-5-)-
902	76	3.6	2332	2	GNNY4F	genome polyprotein
903	76	3.6	2499	1	A30788	mannose 6-phosphat
904	76	3.6	2550	2	B53435	vesicular transpor
905	76	3.6	3716	2	E70969	probable PPE prote
906	76	3.6	4660	2	T42737	gp330 protein prec
907	75.5	3.6	116	2	S22558	Ig heavy chain V r
908	75.5	3.6	146	2	H32536	T-cell receptor al
909	75.5	3.6	275	2	PS0402	basigin type III -
910	75.5	3.6	283	2	F87183	probable exported
911	75.5	3.6	297	2	AG2955	hypothetical prote
912	75.5	3.6	297	2	F98327	hypothetical prote
913	75.5	3.6	312	2	H64560	probable tetracycl
914	75.5	3.6	330	2	I49660	Fc-gamma-1/gamma-2
915	75.5	3.6	342	2	I37527	Ig alpha chain C r
916	75.5	3.6	366	2	A53908	MHC class I histoc
917	75.5	3.6	371	2	S63131	dipeptide ABC tran
918	75.5	3.6	398	2	A39371	hypothetical prote
919	75.5	3.6	459	2	B71417	probable membrane
920	75.5	3.6	502	2	C56205	complement subcomp
921	75.5	3.6	549	2	G69618	hypothetical prote
922	75.5	3.6	605	2	S48940	probable membrane
923	75.5	3.6	636	2	B85075	alcohol dehydrogen
924	75.5	3.6	705	2	C1HURB	complement subcomp
925	75.5	3.6	710	2	B71417	zinc finger protei
926	75.5	3.6	742	2	A49340	alcohol dehydrogen
927	75.5	3.6	761	1	TVHUMB	transforming prote
928	75.5	3.6	769	2	E90158	AAA family ATPase
929	75.5	3.6	790	2	I50178	P-cadherin - chic
930	75.5	3.6	790	2	I51638	cadherin-6B - chic
931	75.5	3.6	796	2	T20393	P-cadherin - Afric
932	75.5	3.6	830	2	T10545	Ig V-region-like B
933	75.5	3.6	866	2	B85075	brevican precursor
934	75.5	3.6	937	1	URHUAP	MHC alpha chain Cr
935	75.5	3.6	974	1	AF0739	Ig alpha chain Cr
936	75.5	3.6	1042	2	T14343	Fc-gamma-1/gamma-2
937	75.5	3.6	1052	2	S49432	zinc finger protei
938	75.5	3.6	1112	2	T01673	transcription fact
939	75.5	3.6	1112	2	T01893	hypothetical prote
940	75.5	3.6	1294	2	C97702	probable athla tr
941	75.5	3.6	1662	2	GNNY2F	neurotrophic recep
942	75.5	3.6	1902	2	A96616	peptidylglycine mo
943	75.5	3.6	2333	1	RWMSAV	exodeoxyribonuclea
944	75.5	3.6	2599	1	A27638	replicase 126K - o
945	75	3.6	132	1	S25744	hypothetical prote
946	75.5	3.6	141	2	S38389	hypothetical prote
947	75.5	3.6	233	2	S01320	cell surface antig
948	75.5	3.6	234	2	D90876	genome polyprotein
949	75.5	3.6	238	2	H72554	unknown protein Fl
950	75.5	3.6	252	2	C85692	T-cell receptor al
951	75.5	3.6	262	2	AC3476	T-cell receptor be
952	75.5	3.6	301	2	B33251	Ig kappa chain pre
953	75.5	3.6	335	2	C81088	Ig lambda chain -
954	75.5	3.6	346	2	AE1931	major tail protein
955	75.5	3.6	360	2	I37120	probable Rieske pr
956	75.5	3.6	362	2	B30345	probable tail comp
957	75.5	3.6	362	2	I37522	probable tail comp
958	75.5	3.6	362	2	I61904	nonspecific protei
959	75.5	3.6	362	2	I54457	alcohol dehydrogen
960	75.5	3.6	362	2	A30345	hypothetical prote
961	75.5	3.6	367	2	S15716	hypothetical prote
962	75.5	3.6	387	2	H65132	MHC class I histoc
963	75.5	3.6	396	2	C95088	MHC class I histoc
964	75.5	3.6	396	2	G97955	MHC class I histoc
965	75.5	3.6	404	2	JQ1531	MHC class I lympho
966	75.5	3.6	450	2	POLJFP	MHC class I histoc
967	75.5	3.6	450	2	S23819	MHC class I lympho
968	75.5	3.6	471	2	B38637	MHC class I histoc
969	75.5	3.6	483	2	A69745	pectate lyase (EC
970	75.5	3.6	496	2	PQ0508	hypothetical 44.3
971	75.5	3.6	496	2	E90181	hypothetical prote
972	75.5	3.6	507	2	AE0473	S-adenosylmethion1
973	75.5	3.6	519	2	F81821	methionine adenosy
974	75	3.6	547	2	T39641	nucleoprotein - he
975	75	3.6	563	2	A70038	gag polyprotein
976	75	3.6	589	2	A34341	gag protein - feli
977	75	3.6	613	2	JC7992	Ras inhibitor (clo
978	75	3.6	630	2	F85074	hypothetical prote

No.			Len	N	Accession	Description
979	75	3.6	632	2	S73431	M6288 homolog D09_
980	75	3.6	669	2	S46519	luciferin-binding
981	75	3.6	669	2	S46518	luciferin-binding
982	75	3.6	686	2	JC7569	Delta-4 protein -
983	75	3.6	808	2	T21129	hypothetical protein
984	75	3.6	997	2	A40812	Ca2+-transporting
985	75	3.6	999	2	A34307	Ca2+-transporting
986	75	3.6	1042	2	B40812	Ca2+-transporting
987	75	3.6	1118	1	A49724	protein-tyrosine-p
988	75	3.6	1144	2	T21223	hypothetical protein
989	75	3.6	1234	2	S72640	endo-1,4-beta-xyla
990	75	3.6	1241	2	S26373	genome polyprotein
991	75	3.6	1277	2	T14152	synaptic scaffoldi
992	75	3.6	1280	2	T29021	hypothetical prote
993	75	3.6	1331	1	XORYDH	xanthine dehydroge
994	75	3.6	1448	2	AI2007	Subtilase family p
995	75	3.6	1622	2	AE1717	probable cell surf
996	75	3.6	2109	1	I50421	aggrecan precursor
997	75	3.6	2124	2	A28452	proteoglycan core
998	75	3.6	2132	1	A55182	aggrecan precursor
999	75	3.6	2415	1	A39086	aggrecan precursor
1000	75	3.6	3216	2	C90538	hypothetical prote
1001	75	3.6	3263	2	E82410	hypothetical prote
1002	75	3.6	3624	2	AD0835	large repetitive p
1003	75	3.6	3712	1	YGCEVC	alpha-aminoadipyl-
1004	75	3.6	3947	2	T52486	ferrichrome sidero
1005	74.5	3.6	115	2	A24891	T-cell receptor al
1006	74.5	3.6	131	2	PQ0059	T-cell receptor be
1007	74.5	3.6	133	2	S57885	probable cell surf
1008	74.5	3.6	135	1	RWHUAV	T-cell receptor al
1009	74.5	3.6	142	1	E64794	ybdQ protein - Esc
1010	74.5	3.6	142	2	F90709	hypothetical prote
1011	74.5	3.6	142	2	B85560	hypothetical prote
1012	74.5	3.6	208	2	B49444	Ig lambda chain (N
1013	74.5	3.6	212	2	C33258	pregnancy-specific
1014	74.5	3.6	223	2	E64205	deoxyribose-phosph
1015	74.5	3.6	235	2	AD1735	hypothetical prote
1016	74.5	3.6	294	2	T05381	hypothetical prote
1017	74.5	3.6	345	1	C72760	probable heme expo
1018	74.5	3.6	348	2	I50107	MHC class I histoc
1019	74.5	3.6	361	2	B90461	hypothetical prote
1020	74.5	3.6	366	1	HLHUW3	MHC class I histoc
1021	74.5	3.6	377	2	A49985	MHC class I histoc
1022	74.5	3.6	445	2	S43492	surface antigen -
1023	74.5	3.6	459	2	T37704	zinc-finger protei
1024	74.5	3.6	476	2	AI0189	exodeoxyribonuclea
1025	74.5	3.6	503	2	AB1933	hypothetical prote
1026	74.5	3.6	536	2	T27668	flagellar basal bo
1027	74.5	3.6	560	2	D30930	hypothetical prote
1028	74.5	3.6	596	2	S32802	DNA-directed RNA p
1029	74.5	3.6	604	2	A43315	ETS domain protein
1030	74.5	3.6	610	2	AE2437	apolipoprotein B -
1031	74.5	3.6	652	2	S52850	prolyl-tRNA synthe
1032	74.5	3.6	657	2	G96560	intermediate filam
1033	74.5	3.6	706	2	G83906	hypothetical prote
1034	74.5	3.6	717	2	D86441	unknown protein [i
1035	74.5	3.6	732	2	B32838	DNA-directed RNA p
1036	74.5	3.6	782	1	T32155	ETS domain protein
1037	74.5	3.6	810	1	A33380	interleukin-4 rece
1038	74.5	3.6	937	2	S78561	CS3 pilin synthesi
1039	74.5	3.6	943	2	B45082	neurotrophic recep
1040	74.5	3.6	946	2	B87316	TonB-dependent rec
1041	74.5	3.6	954	2	I51703	c-kit-related kina
1042	74.5	3.6	1000	1	JE0110	mitotic control pr
1043	74.5	3.6	1013	2	G71460	probable outer mem
1044	74.5	3.6	1025	2	T21319	hypothetical prote
1045	74.5	3.6	1086	2	AH1290	cellobiose-phospho
1046	74.5	3.6	1129	2	S28431	phytochrome B - po
1047	74.5	3.6	1302	2	AC2574	hypothetical prote
1048	74.5	3.6	1333	2	S63403	probable membrane
1049	74.5	3.6	1356	2	T16718	hypothetical prote
1050	74.5	3.6	1446	2	T13018	hypothetical prote
1051	74.5	3.6	1615	2	C75551	glutamate synthase
1052	74.5	3.6	2143	2	G96595	hypothetical prote
1053	74.5	3.6	3890	2	C89921	hypothetical prote
1054	74.5	3.6	4436	2	E71086	giant protein p619
1055	74.5	3.6	4861	1	S71752	hypothetical prote
1056	74	3.5	115	2	A30583	T-cell receptor de
1057	74	3.5	130	2	S08079	Ig kappa chain pre
1058	74	3.5	143	2	S36321	T-cell receptor de
1059	74	3.5	145	2	S36299	T-cell receptor de
1060	74	3.5	217	2	JE0246	Ig lambda chain NI
1061	74	3.5	256	1	QQOMC2	T-cell receptor de
1062	74	3.5	264	2	T26976	T-cell receptor de
1063	74	3.5	270	1	S77085	Ig lambda chain pr
1064	74	3.5	285	2	S36903	Ig mu chain C regi
1065	74	3.5	318	2	C71197	conserved hypothet
1066	74	3.5	327	2	AE3119	class I histocompa
1067	74	3.5	330	2	JC7509	HLA-B*5401 - human
1068	74	3.5	339	2	S20827	MHC HLA-B transmem
1069	74	3.5	341	2	S78042	HLA-B*5502 - human
1070	74	3.5	351	2	C86932	HLA-B*5501 - human
1071	74	3.5	353	2	S24436	MHC class I histoc
1072	74	3.5	354	2	S24436	HLA class I histoc
1073	74	3.5	362	2	I56130	MHC class I protei
1074	74	3.5	362	2	I59633	MHC class I histoc
1075	74	3.5	362	1	I72753	hypothetical prote
1076	74	3.5	362	2	S24434	P-cadherin - bovin
1077	74	3.5	362	2	I72752	adhesin aida-I [im
1078	74	3.5	362	2	I56133	Ig mu chain C regi
1079	74	3.5	365	2	B96260	probable membrane
1080	74	3.5	365	2	B98125	isocitrate dehydro
1081	74	3.5	379	2	T47330	periplasmic-iron-b
1082	74	3.5	379	2	T45768	protein phosphatas
1083	74	3.5	387	2	B98168	recombination prot
1084	74	3.5	425	2	E71982	recF protein [impo
1085	74	3.5	430	2	S50981	4-coumarate-CoA li
1086	74	3.5	450	1	MHDG	hypothetical prote
1087	74	3.5	487	2	AD3643	PE54 protein homol
1088	74	3.5	491	2	IJBOCP	protein dim-1 [imp
1089	74	3.5	517	2	B87644	hypothetical prote
1090	74	3.5	565	2	A90644	transferrin-bindin
1091	74	3.5	617	2	A85495	zinc finger protei
1092	74	3.5	617	2	I38618	glucan 1,3-beta-gl
1093	74	3.5	626	2	T51283	killer cell inhibi
1094	74	3.5	628	1	JC5896	hypothetical prote
1095	74	3.5	635	2	S58154	disintegrin-like m
1096	74	3.5	642	2	S46788	fibroblast growth
1097	74	3.5	659	2	H89581	fibronectin-bindin
1098	74	3.5	666	1	T19474	DNA-directed DNA p
1099	74	3.5	708	2	JN0820	C protein alpha an
1100	74	3.5	711	2	A49123	4-coumarate-CoA li
1101	74	3.5	813	2	G02390	outer membrane ush
1102	74	3.5	814	2	AD0042	enhancing factor (
1103	74	3.5	856	2	AG0859	hypothetical prote
1104	74	3.5	899	2	A46405	pyruvate carboxyla
1105	74	3.5	1020	1	S19661	fibronectin-bindin
1106	74	3.5	1084	1	S33851	hypothetical prote
1107	74	3.5	1117	2	D97227	DNA-directed DNA p
1108	74	3.5	1144	1	T21557	genome polyprotein
1109	74	3.5	1162	2	XOMSDH	xanthine dehydroge
1110	74	3.5	1335	2	S17670	multifunctional am
1111	74	3.5	1452	1	S18644	protein-tyrosine-p
1112	74	3.5	1714	2	S17670	rifamycin polyketi
1113	74	3.5	1763	2	T14705	hypothetical prote
1114	74	3.5	3412	2	GNWVTB	genome polyprotein
1115	73.5	3.5	106	2	PL0267	Ig kappa chain V r
1116	73.5	3.5	108	2	KVRBB5	Ig kappa chain V r
1117	73.5	3.5	111	2	L6HUST	T-cell receptor al
1118	73.5	3.5	111	2	JH0339	Ig kappa chain V r
1119	73.5	3.5	111	2	A20969	Ig lambda chain V r
1120	73.5	3.5	229	2	PS0401	basigin type II -
1121	73.5	3.5	245	2	T14475	basigin -
1122	73.5	3.5	246	2	S38950	hypothetical prote
1123	73.5	3.5	253	2	S43512	GP42/Basigin prote
1124	73.5	3.5	257	2	JX0107	basigin precursor

No.	Score		Len	N	Code	Description
1125	73.5	3.5	284	2	A97203	2-oxoacid ferredox
1126	73.5	3.5	291	2	T30488	hypothetical prote
1127	73.5	3.5	304	2	B88746	protein C18F3.3 [i
1128	73.5	3.5	310	2	JL0119	Fc gamma (IgG) rec
1129	73.5	3.5	316	2	H71231	molybdopterin bios
1130	73.5	3.5	325	2	I54449	MHC class I HLA-Cx
1131	73.5	3.5	348	2	S09273	Ig alpha chain c r
1132	73.5	3.5	351	2	B34595	pregnancy-specific
1133	73.5	3.5	351	2	A97064	D-mannonate hydrol
1134	73.5	3.5	357	2	D82237	UDP-N-acetylenolpy
1135	73.5	3.5	364	1	S68090	actin 8 - Arabidop
1136	73.5	3.5	364	2	OOHUR	opsin, red-sensiti
1137	73.5	3.5	366	2	I68112	MHC class I histoc
1138	73.5	3.5	366	2	F72062	hypothetical prote
1139	73.5	3.5	366	2	A86561	CT449 hypothetical
1140	73.5	3.5	400	2	T34363	hypothetical prote
1141	73.5	3.5	427	2	F81252	NADH2 dehydrogenas
1142	73.5	3.5	427	2	F64064	tolB protein - Hae
1143	73.5	3.5	446	2	S40295	Ig gamma-2a chain
1144	73.5	3.5	482	2	T22754	Ig lambda chain
1145	73.5	3.5	487	1	A49760	funarate hydratase
1146	73.5	3.5	551	2	G84301	hypothetical prote
1147	73.5	3.5	551	2	C70512	hypothetical prote
1148	73.5	3.5	568	2	A89958	acetyl-CoA synthet
1149	73.5	3.5	583	2	T02382	hypothetical prote
1150	73.5	3.5	634	2	S12282	beta-D-glucan exoh
1151	73.5	3.5	659	1	A85854	hypothetical prote
1152	73.5	3.5	659	2	G91009	colicin I receptor
1153	73.5	3.5	663	1	QRE1C	colicin I receptor
1154	73.5	3.5	694	2	F71514	probable translati
1155	73.5	3.5	721	2	T05815	hypothetical prote
1156	73.5	3.5	737	2	T46243	GTP diphosphokinas
1157	73.5	3.5	743	2	D64062	hypothetical prote
1158	73.5	3.5	780	2	A34102	von Willebrand fac
1159	73.5	3.5	780	2	E75625	hypothetical prote
1160	73.5	3.5	794	2	T36672	SOK2 protein - yea
1161	73.5	3.5	886	2	S54016	aconitate hydratas
1162	73.5	3.5	891	2	T19915	probable membrane
1163	73.5	3.5	891	2	S57528	pol polyprotein -
1164	73.5	3.5	899	1	GNMYMM	peptidylglycine mo
1165	73.5	3.5	923	2	S09583	probable ankyrin -
1166	73.5	3.5	934	1	H71274	hypothetical prote
1167	73.5	3.5	1102	2	H84545	endopeptidase la h
1168	73.5	3.5	1127	1	E71156	M polyprotein prec
1169	73.5	3.5	1133	2	GNVUSR	M polyprotein prec
1170	73.5	3.5	1133	2	S12597	fibrinogen-binding
1171	73.5	3.5	1186	2	T28680	hypothetical prote
1172	73.5	3.5	1193	2	T21133	protein F36A2.13 [
1173	73.5	3.5	1259	2	H65233	ytfN protein - Esc
1174	73.5	3.5	1259	1	YGECEF	hypothetical prote
1175	73.5	3.5	1829	2	T24583	enterobactin synth
1176	73.5	3.5	2761	2	T21064	hypothetical prote
1177	73.5	3.5	2899	2	T21546	hypothetical prote
1178	73.5	3.5	2915	2	G87867	protein F36A2.13 [
1179	73.5	3.5	3097	2	T28635	glutamate synthase
1180	73	3.5	107	2	B45722	anti-glycoprotein
1181	73	3.5	113	2	I46637	rearranged T-cell
1182	73	3.5	113	2	B49041	T-cell receptor al
1183	73	3.5	120	2	B25429	T-cell receptor be
1184	73	3.5	126	2	B46538	Ig heavy chain, me
1185	73	3.5	131	1	L6HUEB	Ig lambda chain pr
1186	73	3.5	135	2	S00388	T-cell receptor ga
1187	73	3.5	162	2	E71131	T-cell receptor al
1188	73	3.5	173	2	T27373	peptidylprolyl iso
1189	73	3.5	175	2	T18408	neu differentiatio
1190	73	3.5	186	2	I61783	sodium channel bet
1191	73	3.5	210	2	I49294	CD7 antigen - mous
1192	73	3.5	210	2	I38315	Ig lambda chain V
1193	73	3.5	244	2	S21066	Ig heavy chain C r
1194	73	3.5	247	2	AF0869	probable fimbrial
1195	73	3.5	251	2	T15495	hypothetical prote
1196	73	3.5	253	2	G97267	PHP superfamily hy
1197	73	3.5	267	1	RWMSC8	T-cell receptor al
1198	73	3.5	354	2	B82850	fimbrial adhesin p
1199	73	3.5	362	1	HLHUB8	MHC class I histoc
1200	73	3.5	362	2	A45834	MHC class I histoc
1201	73	3.5	362	2	I61907	MHC class I histoc
1202	73	3.5	362	2	A45850	MHC class I histoc
1203	73	3.5	362	2	I81233	lymphocyte antigen
1204	73	3.5	362	2	I84490	lymphocyte antigen
1205	73	3.5	362	2	A45880	MHC class I histoc
1206	73	3.5	362	2	I54442	MHC class I histoc
1207	73	3.5	365	2	I37482	MHC class I histoc
1208	73	3.5	378	2	S41870	surface antigen -
1209	73	3.5	378	2	C69110	glutamate N-acetyl
1210	73	3.5	402	2	A41070	prolactin receptor
1211	73	3.5	412	2	C72166	A22R protein - var
1212	73	3.5	426	2	G75052	pyruvate kinase (B
1213	73	3.5	478	2	C75052	hypothetical prote
1214	73	3.5	478	2	T24805	protein disulfide-
1215	73	3.5	481	2	JC5378	glutathione-disulf
1216	73	3.5	489	2	T09151	D-alanine activati
1217	73	3.5	499	2	E86782	cystathionine beta
1218	73	3.5	507	2	A48661	hypothetical prote
1219	73	3.5	508	2	B91250	hypothetical prote
1220	73	3.5	521	2	B84746	ABC transporter, A
1221	73	3.5	580	2	AE1088	prolactin receptor
1222	73	3.5	615	2	A36116	hypothetical prote
1223	73	3.5	615	2	A45055	glutamine-fructose
1224	73	3.5	681	2	JC7570	Delta-4 protein -
1225	73	3.5	685	2	A46212	hypothetical prote
1226	73	3.5	687	2	F97279	MEK kinase - mouse
1227	73	3.5	694	2	T13618	TPR-repeat-contain
1228	73	3.5	796	2	D97065	hypothetical prote
1229	73	3.5	885	2	S42841	transketolase [imp
1230	73	3.5	913	2	IJCHCR	T16G12.1 protein -
1231	73	3.5	954	2	AI0438	R-cadherin precurs
1232	73	3.5	998	2	H75005	probable exported
1233	73	3.5	1071	2	B84062	ATP-dependent prot
1234	73	3.5	1115	2	T29012	hypothetical prote
1235	73	3.5	1122	2	T47424	pyruvate carboxyla
1236	73	3.5	1137	2	E86708	hypothetical prote
1237	73	3.5	1144	2	A81983	probable DNA-direc
1238	73	3.5	1177	2	T16594	hypothetical prote
1239	73	3.5	1199	2	T23005	probable ABC trans
1240	73	3.5	1286	2	A88396	hypothetical prote
1241	73	3.5	1286	2	C70044	protein M01E10.2 [
1242	73	3.5	1289	2	B85557	probable phosphoes
1243	73	3.5	1293	2	A90707	enterobactin synth
1244	73	3.5	1345	2	S55669	tegument protein 7
1245	73	3.5	1390	2	TVHUME	hepatocyte growth
1246	73	3.5	1407	2	T00558	probable growth
1247	73	3.5	1437	2	T31093	probable protein-t
1248	73	3.5	1452	2	S17669	protein-tyrosine-p
1249	73	3.5	1484	2	T42632	breast cancer tumo
1250	73	3.5	1487	2	S62048	probable membrane
1251	73	3.5	1615	2	B49502	protein-tyrosine-p
1252	73	3.5	1630	2	A53577	ascites sialoglyco
1253	73	3.5	1767	2	A49502	protein F36A2.13
1254	73	3.5	2118	2	S72705	mycocerosate synth
1255	73	3.5	2142	1	ZLVNPV	genome polyprotein
1256	73		2505	2	XYRTFA	enoyl-[acyl-carrie
1257	73		2813	2	VWHU	von Willebrand fac
1258	73		15281	2	S41309	cyclosporin synthe
1259	72.5	3.5	104	2	S36064	Ig lambda chain -
1260	72.5	3.5	110	2	S23368	T-cell receptor al
1261	72.5	3.5	110	2	S22897	T-cell receptor al
1262	72.5	3.5	111	1	L6HULT	Ig lambda chain V-
1263	72.5	3.5	112	2	L1HUHA	Ig lambda chain V-
1264	72.5	3.5	114	2	I38315	Ig lambda chain V
1265	72.5	3.5	114	2	I38314	T-cell receptor be
1266	72.5	3.5	115	2	S03511	T-cell receptor be
1267	72.5	3.5	115	2	S03510	T-cell receptor be
1268	72.5	3.5	133	1	A25777	T-cell receptor be
1269	72.5	3.5	135	1	RWHUVV	T-cell receptor be
1270	72.5	3.5	135	2	S57877	T cell receptor CK

ID					Accession	Description
1271	72.5	3.5	136	2	I46635	rearranged T-cell
1272	72.5	3.5	140	2	PH0132	Ig lambda chain pr
1273	72.5	3.5	224	2	B81783	hypothetical prote
1274	72.5	3.5	233	2	H03372	4K surface glycop
1275	72.5	3.5	249	2	S69340	Ig heavy chain VHI
1276	72.5	3.5	250	2	D83835	hypothetical prote
1277	72.5	3.5	307	1	RWMSBC	T-cell receptor be
1278	72.5	3.5	312	2	T33344	hypothetical prote
1279	72.5	3.5	315	2	AG2361	hypothetical prote
1280	72.5	3.5	323	1	PEPLBJ	penicillopepsin (E
1281	72.5	3.5	334	2	D83788	UDP-glucose 4-epim
1282	72.5	3.5	365	1	S76914	translation releas
1283	72.5	3.5	365	2	JH0537	class I histocompa
1284	72.5	3.5	366	2	I54430	MHC class I histoc
1285	72.5	3.5	366	2	I61866	gene HLA-C protein
1286	72.5	3.5	366	2	I56034	MHC HLA-Cw2.2 chai
1287	72.5	3.5	408	2	S76830	class I histocompa
1288	72.5	3.5	416	1	KIVKGL	phosphoglycerate k
1289	72.5	3.5	426	2	D42519	hypothetical prote
1290	72.5	3.5	426	2	T37408	cell fusion glycop
1291	72.5	3.5	432	2	T43476	A20R protein - vac
1292	72.5	3.5	460	2	T38608	probable 49.1K pro
1293	72.5	3.5	468	1	VGBBEH	hypothetical prote
1294	72.5	3.5	471	1	PAECA	hypothetical prote
1295	72.5	3.5	487	2	A26731	alkaline phosphata
1296	72.5	3.5	497	2	E86485	cytochrome P450 2C
1297	72.5	3.5	502	2	A83338	hypothetical prote
1298	72.5	3.5	533	1	T34458	RNA polymerase sig
1299	72.5	3.5	553	2	H46329	Ets-related transc
1300	72.5	3.5	568	2	S57830	methyl-accepting c
1301	72.5	3.5	569	2	S41806	hypothetical prote
1302	72.5	3.5	582	2	A46637	eukaryotic-type se
1303	72.5	3.5	605	2	T33913	thymopoietin alpha
1304	72.5	3.5	612	2	B84936	probable translati
1305	72.5	3.5	619	2	A43361	hypothetical prote
1306	72.5	3.5	638	2	T03481	probable transposo
1307	72.5	3.5	641	2	G85043	ATPase - Sulfolobu
1308	72.5	3.5	659	2	G98068	hypothetical prote
1309	72.5	3.5	694	2	G01161	P-cadherin precurs
1310	72.5	3.5	695	2	D71283	hypothetical prote
1311	72.5	3.5	723	2	T30094	hypothetical prote
1312	72.5	3.5	745	2	H85048	hypothetical prote
1313	72.5	3.5	780	1	S43859	genome polyprotein
1314	72.5	3.5	820	1	T14879	platelet-derived g
1315	72.5	3.5	822	1	IJMSCP	hypothetical prote
1316	72.5	3.5	845	2	T12537	hypothetical prote
1317	72.5	3.5	867	2	AD1856	hypothetical prote
1318	72.5	3.5	899	2	B75018	complement C3 prec
1319	72.5	3.5	980	2	A38523	two-component hybr
1320	72.5	3.5	1088	1	PPRRGA	genome polyprotein
1321	72.5	3.5	1106	2	T31742	large repetitive p
1322	72.5	3.5	1131	2	T15787	T-cell receptor be
1323	72.5	3.5	1185	2	T46428	Ig kappa chain V-J
1324	72.5	3.5	1663	1	C3MS	T-cell receptor de
1325	72.5	3.5	1707	2	AH2085	hypothetical prote
1326	72.5	3.5	2271	2	F90073	T-cell receptor al
1327	72.5	3.5	3283	2	AC1018	Ig heavy chain v r
1328	72.5	3.5	111	2	S26255	hypothetical prote
1329	72.5	3.5	111	2	S26256	involved in polyke
1330	72.5	3.5	111	2	S09963	translation elonga
1331	72.5	3.5	136	2	S36304	ribonuclease (EC 3
1332	72.5	3.5	138	2	PN0538	Fc-gamma receptor
1333	72.5	3.5	144	2	A27577	ankyrin-repeat pro
1334	72.5	3.5	171	2	A38237	CD1.1 - mouse
1335	72.5	3.5	259	2	F69678	MHC HLA B71 - huma
1336	72.5	3.5	281	2	S34626	hypothetical prote
1337	72.5	3.5	289	2	S29271	class I histocompa
1338	72.5	3.5	296	1	I46021	Fc-gamma receptor
1339	72.5	3.5	333	2	JC7713	ankyrin-repeat pro
1340	72	3.4	336	2	I49582	CD1.1 - mouse
1341	72	3.4	350	1	I54308	MHC HLA B71 - huma
1342	72	3.4	352	2	G81921	hypothetical prote
1343	72	3.4	354	2	S24437	class I histocompa
1344	72	3.4	362	2	S24435	class I histocompa
1345	72	3.4	362	2	S16789	class I histocompa
1346	72	3.4	365	2	I72170	MHC class I histoc
1347	72	3.4	365	2	S12406	MHC class I histoc
1348	72	3.4	369	2	I32406	glucan endo-1,3-be
1349	72	3.4	386	2	A41950	retrovirus-related
1350	72	3.4	392	2	B87343	probable esterase
1351	72	3.4	397	2	B35878	conserved hypothet
1352	72	3.4	406	2	A42879	class I major hist
1353	72	3.4	416	1	C71097	advanced glycosyla
1354	72	3.4	420	2	T16638	conserved hypothet
1355	72	3.4	436	2	T38221	hypothetical prote
1356	72	3.4	456	2	JC5897	hypothetical serin
1357	72	3.4	466	2	S75369	killer cell inhibi
1358	72	3.4	483	2	T07883	hypothetical prote
1359	72	3.4	505	2	A71564	cellulase (EC 3.2.
1360	72	3.4	520	2	S16989	dihydrolipoamide S
1361	72	3.4	539	2	A32187	interleukin-1 rece
1362	72	3.4	569	2	T28725	hypothetical prote
1363	72	3.4	580	2	T43402	probable protein k
1364	72	3.4	592	2	T23937	protein-tyrosine k
1365	72	3.4	622	2	A61197	6-methylsalicilic
1366	72	3.4	707	2	T02835	long chain fatty a
1367	72	3.4	710	2	T44753	hypothetical prote
1368	72	3.4	733	2	A87168	conserved hypothet
1369	72	3.4	758	2	H75013	hypothetical prote
1370	72	3.4	788	2	S17906	hypothetical prote
1371	72	3.4	828	2	E71417	Ca2+-transporting
1372	72	3.4	828	2	T22367	Ca2+-transporting
1373	72	3.4	915	2	T23937	Ca2+-transporting
1374	72	3.4	974	1	A49714	Ca2+-transporting
1375	72	3.4	994	2	A32792	Ca2+-transporting
1376	72	3.4	997	1	PWRBSC	Ca2+-transporting
1377	72	3.4	997	2	S23444	Ca2+-transporting
1378	72	3.4	997	2	S04651	Ca2+-transporting
1379	72	3.4	997	2	S04652	Ca2+-transporting
1380	72	3.4	997	2	B31982	Ca2+-transporting
1381	72	3.4	1042	2	A31982	hypothetical prote
1382	72	3.4	1042	2	A31981	differentiation-st
1383	72	3.4	1042	2	A33881	M polyprotein - Ha
1384	72	3.4	1043	2	A31982	M polyprotein - Ha
1385	72	3.4	1062	2	A31982	DNA-directed RNA p
1386	72	3.4	1092	2	S09834	DNA topoisomerase
1387	72	3.4	1092	1	JX00312	probable ABC trans
1388	72	3.4	1135	1	GNVUH7	ABC transport prot
1389	72	3.4	1135	1	GNVUHV	RNA polymerase III
1390	72	3.4	1179	2	T04488	MSB2 protein - yea
1391	72	3.4	1210	2	S35548	cell surface glyco
1392	72	3.4	1218	1	AD0293	hypothetical prote
1393	72	3.4	1218	2	T30293	hypothetical prote
1394	72	3.4	1289	2	E90098	nonstructural poly
1395	72	3.4	1306	2	S25370	kinesin family pro
1396	72	3.4	1408	2	H69068	6-methylsalicylic
1397	72	3.4	1461	2	E90696	nonstructural poly
1398	72	3.4	1461	2	A85547	nonstructural poly
1399	72	3.4	1490	2	A56921	protein F21I18.22
1400	72	3.4	1490	2	S72351	probable RTX famil
1401	72	3.4	1695	2	S13178	hypothetical prote
1402	72	3.4	1774	2	S26058	T-cell receptor al
1403	72	3.4	2090	1	MNWVTD	T-cell receptor al
1404	72	3.4	2492	2	A96521	Ig kappa chain V r
1405	72	3.4	2684	2	B85547	T-cell receptor al
1406	72	3.4	5188	2	F90696	Ig kappa chain pre
1407	72	3.4	5291	1	D25733	Ig kappa chain V r
1408	71.5	3.4	102	2	S29588	T-cell receptor de
1409	71.5	3.4	112	2	S22891	T-cell receptor al
1410	71.5	3.4	113	2	S02891	T-cell receptor al
1411	71.5	3.4	139	2	S02410	T cell antigen rec
1412	71.5	3.4	142	2	RWHH7A	major latex protei
1413	71.5	3.4	148	2	S36310	hypothetical prote
1414	71.5	3.4	155	2	A32536	
1415	71.5	3.4	155	2	S58178	
1416	71.5	3.4	238	2	S71257	

ID			Len	N	Accession	Description
1417	71.5	3.4	246	2	PC4397	mucin 3 T10 - huma
1418	71.5	3.4	255	1	S48146	mucin 1 precursor,
1419	71.5	3.4	259	2	S60617	hypothetical prote
1420	71.5	3.4	270	2	G84163	heparin lyase (EC
1421	71.5	3.4	291	2	JQ1562	hypothetical prote
1422	71.5	3.4	319	2	I39966	microbial serine s
1423	71.5	3.4	329	2	JC5168	UDPglucose 4-epime
1424	71.5	3.4	337	2	S65022	glucan endo-1,3-be
1425	71.5	3.4	345	2	I68749	MHC class I lympho
1426	71.5	3.4	349	1	E60096	UDPglucose-hexose-
1427	71.5	3.4	364	2	G64086	glycerophosphodies
1428	71.5	3.4	366	2	I37526	MHC class I histoc
1429	71.5	3.4	366	2	I72113	MHC histocompatibi
1430	71.5	3.4	366	2	I59622	lymphocyte antigen
1431	71.5	3.4	366	1	I38507	MHC class I histoc
1432	71.5	3.4	370	2	A39115	glucan endo-1,3-be
1433	71.5	3.4	370	2	E87729	protein Y23HSA.4 [
1434	71.5	3.4	380	2	T26570	hypothetical prote
1435	71.5	3.4	380	1	A44479	GTP cyclohydrolase
1436	71.5	3.4	384	2	S45545	protein containing
1437	71.5	3.4	398	1	H96967	hypothetical 33.9K
1438	71.5	3.4	426	2	C38850	hypothetical prote
1439	71.5	3.4	426	2	T26563	A1R protein - var
1440	71.5	3.4	428	1	AJR2QD	glutamate-ammonia
1441	71.5	3.4	436	2	A55568	methylcrotonoyl-Co
1442	71.5	3.4	492	2	T47720	pyruvate kinase-11
1443	71.5	3.4	528	2	PC4025	intercellular adhe
1444	71.5	3.4	564	2	T42695	hypothetical prote
1445	71.5	3.4	567	2	F02274	ribulokinase (EC 2
1446	71.5	3.4	570	2	S56132	cellulase (EC 3.2.
1447	71.5	3.4	586	2	T19075	hypothetical prote
1448	71.5	3.4	587	1	A36936	nitrogenase (EC 1.
1449	71.5	3.4	591	2	A36509	oxaloacetate decar
1450	71.5	3.4	591	2	AB0509	oxaloacetate decar
1451	71.5	3.4	640	1	A55073	transforming prote
1452	71.5	3.4	647	2	AB1054	2',3'-cyclic-nucle
1453	71.5	3.4	668	2	A42908	meprin A (EC 3.4.2
1454	71.5	3.4	687	2	T09051	PepA protein - Pse
1455	71.5	3.4	702	2	E69498	kinesin-related pr
1456	71.5	3.4	704	2	I39805	hypothetical prote
1457	71.5	3.4	710	2	A95640	cyclomaltodextrin
1458	71.5	3.4	747	2	B47093	cellulase (EC 3.2.
1459	71.5	3.4	793	2	S34830	kinesin-related pr
1460	71.5	3.4	811	2	PN0689	connectin 1 - chic
1461	71.5	3.4	825	2	AS9296	alpha-L-arabinofur
1462	71.5	3.4	828	2	S52393	beta-galactosidase
1463	71.5	3.4	857	2	T04208	probable anthranil
1464	71.5	3.4	976	1	URRTAP	peptidylglycine mo
1465	71.5	3.4	987	1	H81722	polymorphic membra
1466	71.5	3.4	1005	1	P1VXPJ	RNA 1 protein - pe
1467	71.5	3.4	1025	2	S34839	collagen alpha 1(v
1468	71.5	3.4	1044	2	E86613	ribonucleoside red
1469	71.5	3.4	1044	2	A72010	ribonucleoside-dip
1470	71.5	3.4	1117	2	S63399	probable membrane
1471	71.5	3.4	1137	2	B90734	probable host spec
1472	71.5	3.4	1138	2	D85584	probable tail comp
1473	71.5	3.4	1179	2	C36792	hypothetical prote
1474	71.5	3.4	1226	2	JC7503	protein-tyrosine-p
1475	71.5	3.4	1358	2	T22695	hypothetical prote
1476	71.5	3.4	1441	2	A86685	prophage pil prote
1477	71.5	3.4	1490	2	JC5145	DNA (cytosine-5-)-
1478	71.5	3.4	1582	2	AC1153	adhesin homolog lm
1479	71.5	3.4	1612	2	AB1347	probable peptidogl
1480	71.5	3.4	1680	2	T41628	probable transcrip
1481	71.5	3.4	1815	2	B95942	conserved hypothet
1482	71.5	3.4	1939	2	D97316	probable S-layer p
1483	71.5	3.4	1946	2	AC2141	serine/threonine k
1484	71.5	3.4	2242	2	A57541	pyrimidine synthes
1485	71.5	3.4	2332	1	GNNYF	genome polyprotein
1486	71.5	3.4	3131	2	S39842	enniatin synthetas
1487	71.5	3.4	3191	2	T22945	hypothetical prote
1488	71.5	3.4	6359	2	T31679	bacitracin synthet
1489	71	3.4	87	2	PH1082	Ig light chain V r
1490	71	3.4	98	2	S26911	Ig heavy chain V r
1491	71	3.4	115	1	KVMSL7	Ig kappa chain pre
1492	71	3.4	123	2	S70243	hypothetical prote
1493	71	3.4	166	2	PL0012	Ig heavy chain pre
1494	71	3.4	180	2	G69222	molybdenum formylm
1495	71	3.4	223	2	T33194	hypothetical prote
1496	71	3.4	254	2	S48547	probable membrane
1497	71	3.4	270	2	T03635	probable membrane
1498	71	3.4	287	2	E69901	plastid-lipid-asso
1499	71	3.4	321	2	AC0821	cell wall-binding
1500	71	3.4	336	2	C27658	probable exported
						pregnancy-specific

ALIGNMENTS

RESULT 1
S56749
junctional adhesion molecule precursor - human
N;Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F11
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: A59406; S56749
R;Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; K
J. Immunol. 163, 553-557, 1999
A;Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistribut
A;Reference number: A59406; MUID:99323940; PMID:10395639
A;Accession: A59406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-299 <OZA>
A;Cross-references: UNIPROT:Q9Y624; GB:AAD42050; NID:g5326797; PIDN:AAD42050.1
R;Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.
Biochem. J. 310, 155-162, 1995
A;Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of
A;Reference number: S56749; MUID:95374438; PMID:7646439
A;Accession: S56749
A;Molecule type: protein
A;Residues: 28-49,'X',51-53;62-73,'E',75-103;123,'F',125-130;'FDKDXTIYLNXY';'LT',206,'X'
A;Note: the order of the peptides other than the amino terminus was not determined
C;Genetics:
A;Gene: JAM
C;Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-299/Product: junctional adhesion molecule #status predicted <MAT>

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Query Match             8.5%;  Score 178.5;  DB 2;  Length 299;
Best Local Similarity  26.5%;  Pred. No. 3.5e-06;
Matches   65;  Conservative   36;  Mismatches  93;  Indels  51;  Gaps  11;

Qy    1 MGILLGLILLIGHLLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKRWLVQR 60
          :|| ||| |: |:| :||| |: :  |:|
Db   17 LAILLCSLALGSVTVHS-SEPEVRIPEN------NPVKLSCAY---SGFSSPRVEW---- 62

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK-----VPGDVSLQLSTLEMDDRSHYTCEV 115
         :|||   |: :|: |  |:|                            |||
Db   63 -------KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTRE--DTGTYTCMV 111

Qy  116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQAR-GSPPIS 174
         :  :||  ||   |||
Db  112 SEEGGNSYGEVRVKLIVL----VPPSKPTVNIPS---SATIGNRAVLTCSEBQDGSPPSE 163

Qy  175 YIWYK----QQTN------NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH 222
         :|:|        |||
Db  164 YTWFKDGIVWPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT 223

Qy  223 SDIVK 227
        |:|::
Db  224 SNAVR 228
```

RESULT 2
I38346

elastic titin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998
C;Accession: 138346
R;Label: S.; Kolmerer, B.
Science 270, 293-296, 1995
A;Reference number: A57430; MUID:96026330; PMID:7569978
A;Accession: 138346
A;Title: Titin: giant proteins in charge of muscle ultrastructure and elasticity.
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-7962 <RES>
A;Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g101
C;Genetics:
A;Gene: GDB:TTN
A;Cross-references: GDB:127867; OMIM:188840
A;Map position: 2q31-2q31

Query Match   8.5%;   Score 178; DB 2;   Length 7962;
Best Local Similarity   24.2%;   Pred. No. 0.00025;
Matches 102; Conservative 56; Mismatches 169; Indels 94; Gaps 20;

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Qy     16 DTYGRPILEVPES--VTGPWKGDVNLP----CTYDPLQGYTQVLVRW-------LVQRGSDP  64
             :|::|||:|   ||  :||| |||:|       |   |:|| :     | |||| :
Db    860 DSSGALIVQEPPSFVTKPGSKDV-LPGSAVCLKSTFQGSTPLITRWFKGNKELVSGGSCY 918

Qy     65 VTIFLRDSSGDHIQQAKYQGRLHVSHKYPGDVSLQLSTLEMDDRSHYTCEVTWQTPDG--  122
             | |||||   ||   |   | |||   ||   :||:|:| ||:| |||  || ||
Db    919 IT------------------------KEALESSLELYLVKTSDSGTTYCKVS-NVAGGVE 953

Qy    123 --NQVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQQARGSPPISYIWYK  179
             ||  :| : | |  |  ||    ||  |  ||| || | |  |  ||   :| |||
Db    954 CSANLPVKEPAI--FVEKLEPSQ------LIKKGDATQLACKVTGTPPIKITWFA 1000

Qy    180 QQTNNQEPIK------VATLSTLLFKPAVIADSGSSYFCTAKGQVGSEQHSDIVKFVVKDSS  234
             |  ::   :    | | |||||| |:| ::|: ||   |    :|||:| |:| |||
Db   1001 NDREIKESSKHRMSFVESTAVLRLTDVGIEDSGEYMCEAQNEAGSDHCSSIV--IVKESP 1058

Qy    235 ------KLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAII  288
                  | || |  || |  ||  |  | | | |  :|   | ||    |  | || |||
Db   1059 YFTKEFRPIEVLKEYDVMLLAEVAGTPPFEITW-------FKDNTILRSGRKYKTFIQD 1110

Qy    289 LISLCCM--VVFTMAYIMLCRKTSQQEHVYEAARAHAREAN-------DSGETMR--VAIF  339
             |||| |   |||| ||| |||:||||  :| |  || |||       | |    | ||
Db   1111 HLVSLQILKFVAADAGEYQCRVTNEVGSSICSARVTLREPPSFPIKKIESTSSLRGGTPAAF 1170

Qy    340 ASGCSSDEPTSQNLGNNYSDEPCIGQEYQIIAQINGNYARL-LDTVPLDYEFLATEGKSV  398
              :: |    : |  |  | : ||   |    |  | | ||  |     |    || |:
Db   1171 QATLKGSLPITVTWLKD-SDE--ITEDNIRMTFENNVASLVLSGIEVKH-----DGKXV 1222

Qy    399 C   399
Db   1223 C   1223
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Query Match   8.1%;   Score 170; DB 2;   Length 365;

RESULT 3
JC7780
coxsackie- and adenovirus receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004
C;Accession: JC7780
R;Thoelen, I.; Keyaerts, E.; Lindberg, M.; Van Ranst, M.
Biochem. Biophys. Res. Commun. 288, 805-808, 2001
A;Reference number: JC7780
A;Title: Characterization of a cDNA encoding the bovine coxsackie and adenovirus recepto
A;Contents: Liver
A;Accession: JC7780
A;Molecule type: mRNA
A;Residues: 1-365 <THO>
A;Cross-references: UNIPROT:Q8MWV3; GB:AY033651
C;Comment: This protein serves as the primary adenoviral attachment site on bovine cells

Query Match   8.1%;   Score 170; DB 2;   Length 365;

Best Local Similarity   24.7%;   Pred. No. 2e-05;
Matches 86; Conservative 40; Mismatches 124; Indels 98; Gaps 17;

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Qy      1 MGILLGLILLGHITVDTVGRPILEVPESVTGPWKGD-VNLPCTY-------DPLQGYTQV  52
            :|:|| | || ||  :|| |||   :||| || |  |:||| |       ||| || |
Db      1 MELLIRLFLLLCGVADFTRGLSI-TTPEQMIEKAKGETAYLPCKFTLGPEDQGPLD-----  54

Qy     53 LVKWLVQRGS-----DPVTIFLRDSSGDHIQQAKYQ---GRLHVSHK--VPGDVSLQSTL  103
            ||| |:||      || |||||||||  ||   |    |||| || |  :||| | |:|
Db     55 -IEWLLSPADNQKVDQVILY---SGDKIYDDYYQDLKGRVHFTSNDLKSGDASINVTNL 110

Qy    104 EMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQ---GM  159
            ||||| |||||||||||||| | : |:| | ||||||| |     :||| || |    |
Db    111 QLSDIGTYQCKVXKAPVGNK-----------KIQLTVLVKP-----SGIRCYVDGSEEIN 156

Qy    160 RISLQCQQAR-GSPPISYIWYKQQTNNQEP---IKVATLSTLLFKPAVIADSGSSYFCTAKG  215
            ||||||| |  | ||||| ||||   ||:    |||| |||| ||||| |:|  ||| |
Db    157 DFKLKCEPKEGSLPLRYEWQKLSDSQKLPTSNLPEMTSPVISVKQNASAEYSGYTYTCTVRN 216

Qy    216 QVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETS  275
            | || |:| :| |||||||  | || :|| |  | | |  ||| | | |  ||   | |
Db    217 RVGSDQ------------CLLRLDVVPPSNR-------------------------AGTI 239

Qy    276 AGPGKSLPVFAILILISLCCMVVFTMAYIML CRKTSQQEHVYEAARAH 323
            || ||  ||| |||:|:||||  ||  |   |:   ::  | |:||  |
Db    240 AG-----AVIGTLLALVLALIVP-----------CHKKRREEKYEKEVHH 275
```

RESULT 4
S19247
cell adhesion protein Gp160-Dtrk - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Aug-2004
C;Accession: S19247
R;Pulido, D.; Campuzano, S.; Koda, T.; Modolell, J.; Barbacid, M.
EMBO J. 11, 391-404, 1992
A;Title: Dtrk, a Drosophila gene related to the trk family of neurotrophin receptors, en
A;Reference number: S19247; MUID:92164624; PMID:1371458
A;Accession: S19247
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-1033 <PUL>
A;Cross-references: UNIPROT:Q24327; EMBL:X63453; NID:g7883; PIDN:CAA45053.1; PID:g7884
C;Genetics:
A;Gene: FlyBase:Trk48D
A;Cross-references: FlyBase:FBgn0004839
C;Superfamily: protein kinase homology
C;Keywords: ATP
F;690-1028/Domain: protein kinase homology <KIN>
F;698-706/Region: protein kinase ATP-binding motif

Query Match   6.9%;   Score 144.5; DB 2;   Length 1033;
Best Local Similarity   20.9%;   Pred. No. 0.0067;
Matches 76; Conservative 43; Mismatches 141; Indels 103; Gaps 14;

```
Qy     22 ILEVPES---------VTGPWKGDVNLPC----TYDPLQGYTQVLVKRWLVQRGSDPVTIFLRDSSG  74
            :||:||:         :||| ||| ||       |||| ||| ||    |:|||| || |||||||
Db    370 ILEVIEQLKPVPQPTSKNLELDAVVAKVHCKAQGTPFPQVQWV--RDGENTTL-----P 421

Qy     75 DHIQQAKYQGRLHVSHKYPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITEIR  134
            ||||| |  | | ||| |||| ||| ||:|||||| |||||||||||: |   | :
Db    422 DHVE-------VDANGTLIFRNVNSEHRGNYTCLATNSQGQINATV-AINVV 466

Qy    135 VQKLSVSK------PTVTTGSGYGFTVPQGMRISLQCQQARGSPPISYIWYK------QQTNNQE  186
            |||| ||       ||||| |  | ||  || |||||  |  ||||| |||       ||| |
Db    467 TPKFSVPGVGPIETSEQG----------TVVMHCQAIGDPKPIQWDKDLKYLSENNTDRE 517

Qy    187 PIKVATLSTLLFKPAVIADSGSSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTT  246
            |||| ||||||| |||  ||| ||   | |  ||:| |:|   | || |    |::
Db    518 RFFRLENGTLEIRNVQVEDEGSYGCTIGNSAGLKRED--VQLVVK- 560

Qy    247 MTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAILILISLCCMVVFTMAYIML 306
            ||:||||:|:  |||  | | |  |||   | |||| | ||||:||:||||  ||  |
```

```
Db  561 ----------------------------TTGDGFAPEBSGGDGFLVIRAVLITMTVALAYIVLJVVGLMLW 602
Qy  307 CRKTSQQEHVYEAARAHAREA---NDSGETMRVAIFASGCSSDEPTSQNLGNNYSDEPCIG 364
Db  603 CR----------YRRQRKARLND------LSTKEAGDGPDIAGNGKGSEQPCLS 643
Qy  365 QEY 367
Db  644 KQH 646
```

RESULT 5
B49120
protein-tyrosine kinase (EC 2.7.1.112) dtk2 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
A;Accession: B49120; S18010
R;Shishido, E.; Emori, Y.; Saigo, K.
A;Title: Two FGF-receptor homologues of Drosophila: one is expressed in mesodermal prima
J;FEBS Lett. 289, 235-238, 1991
A;Reference number: S17552; MUID:92008631; PMID:1915852
A;Accession: S18010
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-1052 <SH1>
A;Cross-references: UNIPROT:Q09147; GB:X74031; GB:S63797; NID:g397600; PIDN:CAA52190.1;
A;Experimental source: pupa
A;Note: sequence extracted from NCBI backbone (NCBIN:135151, NCBIP:135153)
R;Shishido, E.; Emori, Y.; Saigo, K.
A;Title: Identification of seven novel protein-tyrosine kinase genes of Drosophila by th
A;Reference number: A49120; MUID:93321617; PMID:8330538
A;Accession: A31917
A;Molecule type: DNA
A;Residues: 869-922 <SH2>
A;Status: not compared with conceptual translation

A;Genetics:
A;Gene: FlyBase:btl; dtk2
A;Cross-references: FlyBase:FBgn0005592
A;Superfamily: protein kinase homology
C;Keywords: ATP; growth factor receptor; phosphotransferase; tyrosine-specific protein k
F;710-1003/Domain: protein kinase homology <KIN>
F;718-726/Region: protein kinase ATP-binding motif

```
Query Match             6.8%;  Score  143.5;  DB  2;  Length  1052;
Best Local Similarity  23.4%;  Pred. No. 0.0082;
Matches  71;  Conservative  44;  Mismatches  119;  Indels  69;  Gaps  14;

Qy   16 DTYGRPILB---------VPESVTGPWKGDVNLPCT-YDP-LQGYTQVLVKWLVQRGSDP 64
Db  130 DLFPQLNESRSLKLLQPLPKTVQRTAGGLFQLNCSPMDPDAKG---VNISWL------ 179

Qy   65 VTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTPDGNQ 124
Db  180 --------HIDTQILGGRGRIKLK---RWSITVGQLQPEDAGSYHCELCVE------QD 221

Qy  125 VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGS---PPISYIWYKQ 181
Db  222 CQRSNPTQLEVISRKHTVPMLKPGYPRNTSIALGDNVSIECLLEDSALEPKITWL-HKGN 280

Qy  182 TNN-------QEPIKVATLSTLLFKPAVI------ADSGSYPCTAKGQVGSEQH 222
Db  281 ADNIDDLLQRLREQSQLPVDVTRLITRMDEPQVLRLGNVLMEDGGWYICIAENQVGRTVA 340

Qy  223 SDIVKFVVKDSSKLLKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSL 282
Db  341 ASYVDLYSPSDTTTVRTTT---TTTVASPIPTASTGEDNDD---DVENPAADASGGVGP-- 393

Qy  283 PVP 285
Db  394 PVP 396
```

RESULT 6
S18252
heparan sulfate proteoglycan - mouse
N;Alternate names: perlecan
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 12-Jul-2004
A;Accession: S18252; A31917; B31917; S66460
R;Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Ha
J;Biol. Chem. 266, 22939-22947, 1991
A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteogl
adhesion molecule.
A;Reference number: S18252; MUID:92078153; PMID:1744087
A;Accession: S18252
A;Molecule type: mRNA
A;Residues: 1-3707 <NOO>
A;Cross-references: UNIPROT:Q05793; EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g2002
R;Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Hass
J;Biol. Chem. 263, 16379-16387, 1988
A;Title: Identification of cDNA clones encoding different domains of the basement membra
A;Reference number: A92680; MUID:89034110; PMID:2972708
A;Accession: A31917
A;Molecule type: mRNA
A;Residues: 940-1601 <NO2>
A;Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253
A;Accession: B31917
A;Molecule type: mRNA
A;Residues: 1870-2600 <NO3>
A;Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301
R;Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem. 231, 551-556, 1995
A;Title: Structural properties of recombinant domain III-3 of perlecan containing a glob
A;Reference number: S66460; MUID:95377282; PMID:7649154
A;Accession: S66460
A;Molecule type: protein
A;Residues: 1272-1274,'X',1276,'X',1278-1279 <SCH>
C;Keywords: glycoprotein
C;Genetics:
A;Residues: 1199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;764-811/Domain: laminin-type EGF-like homology <LEG>
F;1159-1206/Domain: laminin-type EGF-like homology <LEG7>
F;1159-1206/Domain: laminin-type EGF-like homology <LEG7>
F;1563-1610/Domain: laminin-type EGF-like homology <EG7>
F;1613-1668/Domain: laminin-type EGF-like homology <EG7>
F;3163-3198/Domain: EGF homology <EGF>
F;3270-3423/Domain: laminin G repeat homology <EGF7>
F;3464-3492/Domain: EGF homology <EGF7>
F;1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Query Match             6.6%;  Score  139.5;  DB  2;  Length  3707;
Best Local Similarity  25.1%;  Pred. No. 0.083;
Matches  66;  Conservative  31;  Mismatches  105;  Indels  61;  Gaps  14;

Qy   13 LTVDT-----YGRPILEVPSSVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGSDPVTIF 68
Db 2521 LIVDTGTVAPGTPQVQVEES--------ELTLEA-----GHTATL-HCSATGNPPPT-- 2563

Qy   69 LRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTPDGNQVVRD 128
Db 2564 -IHWSKLRAPLPWQHRIEGN-TLVIPRVAQQDSGGQYICNAT------NSAGHT 2608

Qy  129 KITELRVQKLSVSKPTVTTGSGYGFTVPQ-------GMRISLQCQARGSPPISYIWYKQQT 182
Db 2609 EATVV----LHVESPP---------YATIIPEHTSAQPGNLVQLQCLAHGTPPLTYQW--SLV 2656

Qy  183 NNQEPIKVATLSTLL-FKPAVIADSGSYPCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKT 241
Db 2657 GGVLPEKAVVRNQLLRLEPTVPEDSGRYRCQVSNRVGSAE--APAQVLVQGSSSNLPDTS 2714

Qy  242 ----EAPTTMTYPLKATSTVKQS 260
Db 2715 IPGGSTPTVQVTPQLETRNIGAS 2737
```

RESULT 7

PFHUGB
platelet-derived growth factor receptor beta precursor - human
N;Contains: protein-tyrosine kinase
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
A;Accession: A28206; A31195; A38268; A31925; B31925; C31925
R;Gronwald, R.G.K.; Grant, F.J.; Haldeman, B.A.; Hart, C.E.; O'Hara, P.J.; Hagen, F.S.;
Proc. Natl. Acad. Sci. U.S.A. 85, 3435-3439, 1988
A;Title: Cloning and expression of a cDNA coding for the human platelet-derived growth f
A;Reference number: A28206; MUID:88217915; PMID:2835772
A;Molecule type: mRNA
A;Residues: 1-1106 <GRO>
A;Cross-references: UNIPROT:P09619; GB:J03278; NID:g189729; PIDN:AAA36427.1; PID:g189732
R;Claesson-Welsh, L.; Eriksson, A.; Moren, A.; Severinsson, L.; Ek, B.; Oestman, A.; Bet
Mol. Cell. Biol. 8, 3476-3486, 1988
A;Title: cDNA cloning and expression of a human platelet-derived growth factor (PDGF) re
A;Reference number: A31195; MUID:89096941; PMID:2850496
A;Molecule type: mRNA
A;Residues: 1-240, 'D', 242-1106 <CLA>
A;Cross-references: GB:M21616; NID:g189730
R;Pattanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
A;Reference number: A38268; MUID:91062389; PMID:2247464
A;Molecule type: DNA
A;Accession: A38268
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1047-1106 <RO3>
A;Accession: C31925
A;Status: not compared with conceptual translation
A;Residues: 901-932 <RO2>
A;Accession: B31925
A;Status: not compared with conceptual translation
A;Residues: 676-727 <ROB>
A;Accession: A31925
A;Molecule type: DNA
A;Residues: 828-884 <PAR>
R;Roberts, W.M.; Look, A.T.; Roussel, M.F.; Sherr, C.J.
Cell 55, 655-661, 1988
A;Title: Tandem linkage of human CSF-1 receptor (c-fms) and PDGF receptor genes.
A;Reference number: A90908; MUID:89028677; PMID:2846185
A;Accession: A31925
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Cross-references: OMIM:173410
A;Map position: 5q31-5q32
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C;Keywords: ATP; autophosphorylation; glycoprotein; growth factor receptor; heterodimer;
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-1106/Product: platelet-derived growth factor receptor beta #status predicted <MAT>
F;33-531/Domain: extracellular #status predicted <EXT>
F;47-102/Domain: immunoglobulin homology <IMM1>
F;142-192/Domain: immunoglobulin homology <IMM2>
F;228-293/Domain: immunoglobulin homology <IMM3>
F;429-510/Domain: immunoglobulin homology <IMM4>
F;532-555/Domain: transmembrane #status predicted <TMM>
F;556-1106/Domain: intracellular #status predicted <INT>
F;598-965/Domain: protein kinase homology <KIN>
F;606-614/Region: protein kinase ATP-binding motif
F;606,89,103,215,230,292,307,354,471,468,479/Binding site: carbohydrate (Asn) (covalent)
F;54-100,149-190,235-508/Disulfide bonds: #status predicted
F;614/Active site: Lys #status predicted
F;857/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

Query Match   6.6%;   Score 139;   DB 1;   Length 1106;
Best Local Similarity   19.7%;   Pred. No. 0.019;

Matches   85;   Conservative   59;   Mismatches   126;   Indels   162;   Gaps   19;

Qy   23 LEVPESVTGPW------------------KGDVNLPCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSG 74
                : | ::::: ||:| ::|||| :|:||:||:||| :|||::|||||||
Db   145 ITIPCRVTDPQLVVTLHEKKGGDVALPVYDHQRGFSGI------------------------------ 182

Qy   75 DHIQQAKYQGRLHVSHKYPGDVSLQLSTLEMDRSHYTCEVTWQTPDGNQVVRDKITELR 134
                 ::||:|:| || :|||:|||||:|||||||||||||:||||:||::| : |:|:|
Db   183 ------------FEDRSYICKTIIGD------------REVDSDAYY------------ 210

Qy   135 VQKLSVSKPTVTTGSGYGFTVPGGMRISLQCQQARGSPPISYIW-YKQQTNNQ--EPIKVA 191
                |:||:||||||||:|||||:||||||||:||:|||||:||| ||| :|||||||
Db   211 VSSINVSVNAVQT-----VVRQGENITLMCIVIGNEVVNFEWTYPRKESGRLVEPVTDF 264

Qy   192 TL-------STTLLFKPAVIADSGSSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAP 244
                ::   :::|: :|:| :::   :::::::::   VYEAARAHAREA 327
Db   265 LLDMPYHIRSILHIPSAELEDSGTYTCNVTESVNDHQDEKAINITVVESG-YVRLLGEVG 323

Qy   297 VVFTMAYI----MLCRKTSQQEH-----------------------------VYEAARAHAREA 327
                : ::   :|:   ::|||||:||
Db   371 NVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVLRLSESHP---- 427

Qy   324 TLQPAELHRSRTLQVVFEAYPPPTVLWFKD-NRTLGDSSAGE---------------IALSTR 370
                ::   ::::::::|:||:|||||:|||||| |||||:|| ||:|||
Db   428 -DSGEQTVRCRGRGMPQENIIWSACRDLKRCPRELPPTLLGNSSEBESQLETNVTYWEEB 486

Qy   328 NDSGE-TMRVA----------------IFASGC----------------SSDEPTSQNLGNNYSDEP 361
                || ||:| ||:|| :|||||:||::|||
Db   371 NVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVLRLSESHP--- 427

Qy   362 CIGQEYQIIAQI 373
                |:|||::|||:
Db   487 --QEFEVVSTL 495

RESULT 8

PN0568
connectin 3B - chicken (fragment)
N;Alternate names: Cn3B protein
C;Species: Gallus gallus (chicken)
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
A;Accession: PN0568
R;Maruyama, K.; Endo, T.; Kume, H.; Kawamura, Y.; Kanzawa, N.; Nakauchi, Y.; Kimura, S.;
Biochem. Biophys. Res. Commun. 194, 1288-1291, 1993
A;Title: A novel domain sequence of connectin localized at the I band of skeletal muscle
A;Reference number: PN0568; MUID:93356802; PMID:8352787
A;Accession: PN0568
A;Molecule type: mRNA
A;Residues: 1-1323 <MAR>
A;Cross-references: UNIPROT:Q08476; DDBJ:D16541; NID:g391629; PID:d1004495; PID:g391630
A;Experimental source: skeletal muscle
C;Comment: This protein string-like single molecule spans from the Z line to the M line

Query Match   6.6%;   Score 138.5;   DB 2;   Length 1323;
Best Local Similarity   21.4%;   Pred. No. 0.026;

Matches   61;   Conservative   38;   Mismatches   117;   Indels   69;   Gaps   10;

Qy   22 ILEVPESV----TGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSGDHIQ 78
                |||:|:| :||:|| |:||||:||||||:||:|:|:||||:|:||:|::|||::
Db   143 ILEIPNSKLEDSQGYSCHIENDSGQDNCHGAITILEPPYFVVTILEPVQVTVGDSASLQCQ 202

Qy   79 QAK-------YQG------RLHVSHKYPGDVSLQLSTLEMDRSHYTCEVTWQTP 120
                |:| |:| |||||||:|||||:|||||||||||||:||||:||
Db   203 VAGTPEMIVSWYGDTKLRGTATVKMIFKNQV---ATLVFSQVDSDDSGEYICKVENTVG 259

Qy   121 DGNQ------VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPGGMRISLQCQQARGSPPISY 175
                ||:| ::|::||::|:||:||||||||:|||||:||||||||||:||:|||||:|||
Db   260 EATSSSLLTVQERKLPPSFTRKLRDVHETV------------GLPVTFDCGIAGSEPIEV 307

Qy   176 IWYKQQTNNQEPIKVAT--LSTLLFKPAVIADS---GSYFCTAKGQVGSEQHSDIVKFVV 230
                || :|||||||::||| ::::| ||:||| :||||||||||||||:|||||
Db   308 SWFKDNRVKEDYNVHISFIDNVAILQILKTDKSLMGQYTCPASNAIGT------A 357

```
Qy    231  KDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETS 275
                 |: :| |  | || |  ||
Db    358  SSSGKLVLTEGKTPFFDTPI------------------TPVDGIGESA 389
```

RESULT 9
T42633
connectin/titin - chicken (fragment)
C;Species: Gallus gallus (chicken)
A;Accession: T42633
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
A;Residues: 1-4162 <YAJ>
R;Yajima, H.; Ohtsuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.; Ma
Biochem. Biophys. Res. Commun. 223, 160-164, 1996
A;Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/titin re
A;Reference number: Z22221; MUID:96254045; PMID:8660363
A;Cross-references: UNIPROT:Q98918; EMBL:D83390; NID:g1511029; PIDN:BAA11908.1; PID:g151
A;Experimental source: breast muscle
C;Keywords: skeletal muscle

```
Query Match           6.6%;  Score 138.5; DB 2;  Length 4162;
Best Local Similarity  21.4%;
Matches  61;  Conservative  38;  Mismatches 117;  Indels  69;  Gaps  10;

Qy    22  ILEVPESV--TGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSGDHIQ 78
Db  3895  ILEIPNSKLEDQQGYSCHIENDSGQDNCHGAITILEPPYFVTPLEPVQVTVGDSASLQCQ 3954

Qy    79  QAK------YQG--------RLHVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120
Db  3955  VAGTPEMIVSWYKGDTKLRGTATVKMHFKNQV--ATLVFSQVDSDDSGGEYICKVENTVG 4011

Qy   121  DGNQ-----------VVRDKITELRVQKLSVSKPTVTTGSYGFTVPQGMRISLQCQOARGSPPISY 175
Db  4012  EATSSSLITVQERKLPPSFTRKLRDVHETV------GLPVTFDCGIAGSEPIEV 4059

Qy   176  IWYKQQTNNQEPIKVAT--LSTLLFKPAVIADS--GSYFCTAKGQVGSEQHSDIVKFVV 230
Db  4060  SWFKDNVRVKEDYNVHTSFIDNVAILQILKTDKSLMGQYTCTASNAIGT-------A 4109

Qy   231  KDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETS 275
Db  4110  SSSGKLVLTEGKTPFFDTPI-----------------TPVDGIGESA 4141
```

RESULT 10
T08678
hypothetical protein DKFZp564I1922.1 - human (fragment)
C;Species: Homo sapiens (man)
A;Accession: T08678
A;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16469
A;Accession: T08678
A;Molecule type: mRNA
A;Residues: 1-584 <WAM>
A;Cross-references: UNIPROT:Q9Y3Y8; EMBL:AL049946
A;Experimental source: fetal brain; clone DKFZp564I1922
C;Genetics:
A;Note: DKFZp564I1922.1

```
Query Match            6.5%;  DB 2;  Length 584;
Best Local Similarity  22.4%;
Matches  53;  Conservative  37;  Mismatches  99;  Indels  48;  Gaps  8;

Qy    35  GDVNLPCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYPG 94
Db    15  GDLKVDCV---ATGLPNPEISWSLPDGSLVNSFMQSDDSGGRTKR------YVVFN 61
```

```
Qy    95  DVSLQLSTLEMDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKP-TVTTGSYGF 153
Db    62  NGTLYFNEVGMREGDYTCFAE------NQVGKD---EMRVRVKVTAPATIRNKTCLAV 112

Qy   113  QVPYGDVTVVACEAKGEPMPKVTWLSPTNKVIPTSSEKYQIYQDGTLIQKAQRSDSGNY 172

Qy   173  TCLVRNSAGEDRKTVWIHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAEGIPT 229
Db         -----SDIVKFVVKDSSKLLKTKTEA-PT 245

Qy   210  FCTAKGQVGSEQH----------------- 229

Qy   154  TVPQGMRISLQCQOARGSPPISYIWY------KQQTNNQEPIKVATLSTLLFKPAVIADSGSY 209
```

RESULT 11
T20992
hypothetical protein F15G9.4a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
A;Molecule type: DNA
A;Residues: 1-5175 <WIL>
A;Cross-references: UNIPROT:Q8I0L3; EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F1
A;Experimental source: clone F15G9
A;Accession: T24733
A;Status: preliminary; translated from GB/EMBL/DDBJ
R;Kershaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19929
A;Accession: T24733
A;Molecule type: DNA
A;Residues: 1-5175 <WI2>
R;Sulston, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19355
A;Accession: T20992
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
A;Experimental source: clone T09B9
C;Genetics:
A;Gene: F15G9.4a
A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3303/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/

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Query Match            6.4%;  Score 133.5; DB 2;  Length 5175;
Best Local Similarity  22.9%;
Matches  48;  Conservative  36;  Mismatches  93;  Indels  33;  Gaps  6;

Qy    76  HIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTPDGNQVVRDKITELRV 135
Db  2796  HAHDESVQNGVITSKYAANEKTLNVTNIQLDDEGFYYC-----TAVNEAGITKFFKLIV 2850

Qy   136  ----------QKLSVSKPTVTTGSYGFTVPQGMRISLQCQOARGSPPISYIWYKQQTNQE 186
Db  2851  IETPYFLDQKU------------YPIILGKRLTLDCSATGTPPPTILFMKDGKRLNE 2896

Qy   187  PIKVATL-STLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVV--KDSSKLLKTKTEA 243
Db  2897  SDEVDIIGSTLVIDNPQKEVEGRYTCIAENKAGRSEKDMMVEVLLPPKLSKEWINVEVQA 2956

Qy   244  --PTTMTYPLKATSTVKQSWDWTTDMDGYL 271
Db  2957  GDPLTLECPIEDTSGVHITWSRQFGCKDGQL 2986
```

RESULT 12
T43290
hemicentin precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
A;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
R;Vogel, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998

A;Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ—
A;Reference number: Z22396
A;Accession: T43290
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5198 <VOG>
A;Cross-references: UNIPROT:O76518; EMBL:AF074901; PIDN:AAC26792.1
R;Sulston, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: 219355
A;Accession: T20993
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5198 <WI1>
A;Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
R;Kershaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: 219929
A;Accession: T24734
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5198 <WI2>
A;Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
C;Genetics:
A;Gene: him-4; F15G9.4b
A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
1; 4225/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;

Query Match   Best Local Similarity   22.9%;   Score 133.5;   DB 2;   Length 5198;
Matches   48;   Conservative   36;   Mismatches   93;   Indels   33;   Gaps   6;

Qy   76   HIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTPDGNQVVRDKITELRV   135
           :||:|| |: |:|: ||: :|| | |||:| ||
Db   2796   HAHDESVQNGVITSKYAANEKILNVTNIQLDDEGFYYC------TAVNEAGITKKFFKLIV   2850

Qy   136   -------QKLSVSKPFVTTGSGYGFTVPQGMRISLQCCQARGSPPISYIWYKQQTNNQE   186
           | : ||| | |||||||||||| :: ||: :
Db   2851   IETPYFLDQQKL------YPIILGKRLTLDCSATGTPPPILFMKDGKRLNE   2896

Qy   187   PIKVATL-STLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVV--KDSSKLLKTKTEA   243
           :|||: |:|||||: |||: ||||| ||
Db   2897   SDEVDIGSTLVIDNPQKEVEGRYTCIAENKAGRSEKDMMVEVLLPPKLSKEWINVEVQA   2956

Qy   244   --PTTMTYPLKATSTVKQSWDWTTDMGYL   271
           ||:| :||
Db   2957   GDPLTLECPIEDTSGVHITWSRQFGKDGQL   2986

RESULT 13
C42632
cell adhesion molecule apCAM (clone d12) - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: C42632
R;Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
Science 256, 638-644, 1992
A;Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plastic
A;Reference number: A42632; MUID:92263095; PMID:1585176
A;Accession: C42632
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-765 <MAY>
A;Cross-references: UNIPROT:Q97WA4
A;Experimental source: CNS
A;Note: sequence extracted from NCBI backbone (NCBIP:1013351)
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

Query Match   6.3%;   Score 132.5;   DB 2;   Length 765;

RESULT 14
B42632
cell adhesion molecule apCAM (clone d15) - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B42632
R;Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
Science 256, 638-644, 1992
A;Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plastic
A;Reference number: A42632; MUID:92263095; PMID:1585176
A;Accession: B42632
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-812 <MAY>
A;Cross-references: UNIPROT:Q97WA5
A;Experimental source: CNS
A;Note: sequence extracted from NCBI backbone (NCBIP:1013346)
A;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

Query Match   6.3%;   Score 132.5;   DB 2;   Length 812;
Best Local Similarity   20.7%;   Pred. No. 0.041;
Matches   54;   Conservative   31;   Mismatches   63;   Indels   113;   Gaps   10;

Qy   104   EMDRSHYTCEV-------------TWQTPDGNQVVRDKITELRVQKLSVSKPT------VTTGSG   150
           :||: :| || ||: ||||:| || |
Db   230   KVGDEVKITCQATGVPPPTYQFKGDVVWTDEMVNNGVLTINPLKTTDQATYICIATNKG   289

Qy   151   YGFT----------VP------------QGMRISLQCCQARGSPPISYIW----------   177
           :|: ||||||||||||||
Db   290   -GFAESSNTLDVKVPPTIEDMEETYDAVSGQELTITCTAKGDPEPSVIWKKKDGPQSASTD   348

Qy   178   -----YKQQTNNQEPIKVATLST-LLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKF   228
           :|: ||||||||| ||: |||||| ||
Db   349   GIVNKGPTYEKVGSSNQNDMEEKTVAQHMTFKPVTYQDAGTYICTAFSLVGSANKT--VKL   406

Qy   229   VVK---------------------------------DSSKLLKTKT   241
           :: ::
Db   407   TVQYKPNFDTDFKEREFFGWRGHKANLTCQANANPVATIEWYMPDAENPDDYSKAVRIPN   466

Qy   242   EAPTTMTYPLKATSTVKQSWD   262
           ::|| |||
Db   467   EAPYTI-------NMLQKWD   479

RESULT 15
A42632
cell adhesion molecule apCAM (clone d19) - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

Query Match

Best Local Similarity   20.7%;   Pred. No. 0.037;   DB 2;   Length 5198;

Qy   104   EMDRSHYTCEV-------------TWQTPDGNQVVRDKITELRVQKLSVSKPT------VTTGSG   150
           :||: :| || ||: ||||:| || |
Db   230   KVGDEVKITCQATGVPPPTYQFKGDVVWTDEMVNNGVLTINPLKTTDQATYICIATNKG   289

Qy   151   YGFT----------VP------------QGMRISLQCCQARGSPPISYIW---------   177
           :|: ||||||||||||||
Db   290   -GFAESSNTLDVKVPPTIEDMEETYDAVSGQELTITCTAKGDPEPSVIWKKKDGPQSASTD   348

Qy   178   -----YKQQTNNQEPIKVATLST-LLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKF   228
           :|: ||||||||| ||: |||||| ||
Db   349   GIVNKGPTYEKVGSSNQNDMEEKTVAQHMTFKPVTYQDAGTYICTAFSLVGSANKT--VKL   406

Qy   229   VVK---------------------------------DSSKLLKTKT   241
           :: ::
Db   407   TVQYKPNFEDTDFKEREFFGWRGHKANLTCQANANPVATIEWYMPDAENPDDYSKAVRIPN   466

Qy   242   EAPTTMTYPLKATSTVKQSWD   262
           ::|| |||
Db   467   EAPYTI-------NMLQKWD   479

C;Accession: A42632
R;Mayford, M.; Barzilai, A.; Keller, F.; Schacher, S.; Kandel, E.R.
Science 256, 638-644, 1992
A;Title: Modulation of an NCAM-related adhesion molecule with long-term synaptic plastic
A;Reference number: A42632; MUID:92263095; PMID:1585176
A;Accession: A42632
A;Molecule type: nucleic acid
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-932 <MAY>
A;Molecule type: nucleic acid
A;Cross-references: UNIPROT:Q9TWA6
A;Experimental source: CNS
A;Note: sequence extracted from NCBI backbone (NCBIP:101342)
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

Query Match   6.3%;   Score 132.5; DB 2;   Length 932;
Best Local Similarity   20.7%;   Pred. No. 0.049;
Matches   54; Conservative   31;   Mismatches   63;   Indels   113;   Gaps   10;

Qy   104 EMDDRSHYTCEV----------------TWQTPDGNQVVRDKITELRVQKLSVSKPT-------VTTGSG 150
          ::   :|:| |::
Db   230 KVGDEVKITCQATGVPPPYQFKKGDVMVTDEMVNNGVLTINPLKTTDQATYTCIATNKG 289

Qy   151 YGFT--------VP------------QGMRISLQCQARGSPPISYIW------------ 177
          |:| || ::| :|:| ||
Db   290 -GPAESSNTLDVKVPPTIEDMEETYDAVSGQELTITCTRAKGDPEPSVIWKKDGPQSASTD 348

Qy   178 ------------YKQQTNNQEPIKVATLST-LLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKP 228
                      :|:| || :|: | || ||||| ||
Db   349 GIVNKGPTYEKVGSNQNDMEEKTVAQHMTFKPVTYQDAGTYICTAPSLVGSANKT--VKL 406

Qy   229 VVK---------------------------------------DSSKLLKTKT 241
          ||: || ::
Db   407 TVQYKPNFDTDFKEREFFGWRGHKANLTCQANANPVATIEWYMPDAENPDDYSKAVRIPN 466

Qy   242 EAPITMTYPLKATSTVKQSND 262
          ||:| || :: ||
Db   467 EAPVTI------------NMLQKWD 479

Search completed: March 2, 2005, 15:22:22
Job time : 42 secs

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OM protein - protein search, using sw model

Copyright (c) 1993 - 2005 Compugen Ltd.
GenCore version 5.1.6

Run on: March 2, 2005, 15:20:17 ; Search time 66 Seconds
(without alignments)
3095.751 Million cell updates/sec

Title: US-10-633-008-32
Perfect score: 2098
Sequence: 1 MGILLGLLLLGHITVDTYGR.........LLDTVPLDYEFLATEGKSVC 399

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :   1: uniprot_sprot:*
                2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length	DB	ID	Description
1	2098	100.0	399	2	Q9Y279	homo sapien
2	1688	80.5	321	2	Q6UXI4	homo sapien
3	840	40.0	280	2	Q80WA3	mus musculu
4	178.5	8.5	299	1	JAM1_HUMAN	homo sapien
5	178	8.5	7962	2	Q10465	homo sapien
6	178	8.5	34350	2	Q8WZ42	homo sapien
7	177	8.4	319	1	A33_HUMAN	homo sapien
8	170.5	8.1	292	2	Q66I72	brachydanio
9	170	8.1	365	2	Q8WMV3	bos taurus
10	169.5	8.1	298	1	JAM1_BOVIN	bos taurus
11	168	8.0	300	2	Q8VC39	mus musculu
12	168	8.0	319	2	Q9TU79	sus scrofa
13	167.5	8.0	319	2	Q9TU80	canis famil
14	167	8.0	300	1	JAM1_MOUSE	mus musculu
15	167	8.0	300	2	Q9JHY1	rattus norv
16	165	7.9	335	2	Q9PWR4	gallus gall
17	163	7.8	335	2	Q9YGH1	gallus gall
18	161	7.7	319	1	A33_MOUSE	mus musculu
19	160	7.6	291	2	Q66I15	xenopus tro
20	159	7.6	332	2	Q6P359	xenopus tro
21	159	7.6	344	2	Q9UKV4	homo sapien
22	159	7.6	365	1	CXAR_HUMAN	homo sapien
23	158.5	7.6	373	2	Q9H6B4	homo sapien
24	157	7.5	365	1	P78310	homo sapien
25	156.5	7.5	335	2	Q9YGV5	gallus gall
26	156	7.4	289	2	Q7ZZ48	brachydanio
27	154.5	7.4	512	2	Q7ZWT0	xenopus lae
28	154.5	7.4	5636	2	Q96DN8	homo sapien
29	152.5	7.3	372	2	Q8KIG0	rattus norv
30	151	7.2	390	2	Q96RW7	homo sapien
31	150	7.1	1395	2	O44924	drosophila
32	149.5	7.1	344	2	Q9R067	rattus norv
33	149.5	7.1	358	2	Q9R066	rattus norv
34	149	7.1	373	2	Q920S5	mus musculu
35	149	7.1	1395	2	Q7KYK3	drosophila
36	148	7.1	1429	2	Q9W213	drosophila
37	148	7.1	373	2	Q8R373	mus musculu
38	145.5	6.9	1271	2	Q6U7I4	brachydanio
39	145.5	6.9	3410	2	Q7TN00	rattus norv
40	145	6.9	3950	2	Q7YRF5	canis famil
41	144.5	6.9	1033	2	Q7P8J8	anopheles g
42	144.5	6.9	1033	2	Q9QE16	anopheles g
43	144.5	6.8	537	1	FGR2_DROME	drosophila
44	143.5	6.8	403	2	Q9V643	drosophila
45	143.5	6.8	1052	2	Q9V08	drosophila
46	143	6.8	1316	2	Q9D147	drosophila
47	143	6.8	448	2	Q9QE16	anopheles g
48	142.5	6.8	372	2	Q8IGA5	drosophila
49	142.5	6.8	396	2	Q9Y50	mus musculu
50	142.5	6.8	523	2	Q99N28	m nectin-11
51	142.5	6.8	1117	2	Q80E2	mus musculu
52	142	6.8	714	2	Q62PB6	mus musculu
53	142	6.8	305	2	Q62P86	gallus gall
54	141.5	6.7	4071	2	Q6KDZ1	gallus gall
55	141	6.7	1052	2	Q8VIM2	mus musculu
56	140.5	6.7	352	2	Q91W66	drosophila
57	140.5	6.7	359	2	Q9VUC8	drosophila
58	140.5	6.7	359	1	LACH_DROME	drosophila
59	140.5	6.7	365	2	Q9V6C2	drosophila
60	140.5	6.7	365	2	Q24372	drosophila
61	140.5	6.7	397	2	Q9VUC8	drosophila
62	140	6.7	308	2	P97792	mus musculu
63	140	6.7	332	2	P97269	cavia porce
64	140	6.7	1662	2	Q9VQY0	drosophila
65	139.5	6.7	413	2	P09619	homo sapien
66	139.5	6.6	3707	1	PGBM_MOUSE	mus musculu
67	139	6.6	330	2	P97269	cavia porce
68	139	6.6	377	2	Q9VQY0	drosophila
69	139	6.6	1106	1	PGDR_HUMAN	homo sapien
70	139	6.6	1479	2	Q7KQT5	drosophila
71	139	6.6	1482	2	Q9V4Y0	drosophila
72	138.5	6.6	310	2	Q9BX67	homo sapien
73	138.5	6.6	310	1	JAM3_HUMAN	homo sapien
74	138.5	6.6	423	2	Q9DBB7	mus musculu
75	138.5	6.6	569	2	Q8BU57	mus musculu
76	138.5	6.6	1323	1	SILF_MOUSE	mus musculu
77	138.5	6.6	4162	2	Q08476	gallus gall
78	138	6.6	285	2	Q9D780	mus musculu
79	138	6.6	298	2	Q9D780	mus musculu
80	138	6.6	360	2	Q80484	brachydanio
81	138	6.6	463	1	HPL3_HUMAN	homo sapien
82	138	6.6	697	2	Q96B86	xenopus lae
83	138	6.6	1059	2	Q66I72	brachydanio
84	138	6.6	1119	2	Q8NC72	homo sapien
85	138	6.6	2022	2	Q6UXM1	homo sapien
86	137.5	6.6	309	2	Q6UXL7	homo sapien
87	137.5	6.6	310	2	Q6UXL17	homo sapien
88	137.5	6.6	461	2	Q7KQQ5	drosophila
89	137.5	6.6	749	2	Q96FLL	homo sapien
90	137.5	6.6	902	2	Q9D1M9	mus musculu
91	137.5	6.6	903	2	Q9EPK4	m junctiona
92	137.5	6.6	903	2	Q13854	homo sapien
93	137.5	6.6	...	2	Q96FD9	drosophila
94	137.5	6.6	...	2	Q8IQ17	drosophila
95	137.5	6.6	...	2	Q96FD8	drosophila
96	137.5	6.6	...	2	Q9VQY1	drosophila
97	137	6.5	1531	2	Q96N34	drosophila
98	137	6.5	398	2	Q8N126	homo sapien
99	137	6.5	432	2	Q9VY33	drosophila
100	137	6.5	450	2	Q6UFP1	homo sapien
101	137	6.5	...	2	Q6UX10	homo sapien
102	137	6.5	...	2	Q8MKM6	drosophila
103	137	6.5	...	2	Q9NBA1	drosophila
104	137	6.5	2019	2	Q8MKM8	drosophila

No.	Score		Length	N	Accession	Organism
105	137	6.5	2828	2	Q9NR99	homo sapien
106	136.5	6.5	394	2	Q7ZXX1	xenopus lae
107	136.5	6.5	487	2	Q7T2H2	gallus gall
108	136.5	6.5	1624	2	Q63ZG4	xenopus lae
109	136.5	6.5	1827	2	Q9VSG5	drosophila
110	136	6.5	283	2	Q9VT76	drosophila
111	136	6.5	316	2	Q7TPB4	rattus norv
112	136	6.5	584	2	Q9Y3Y8	homo sapien
113	136	6.5	1431	2	Q80U60	mus musculu
114	135.5	6.5	298	2	Q8C5K9	mus musculu
115	135.5	6.5	439	2	O57349	gallus gall
116	135.5	6.5	632	2	Q6ZRK5	homo sapien
117	135.5	6.4	394	2	Q925F2	mus musculu
118	135	6.4	838	2	Q90YM1	brachydanio
119	135	6.4	1235	2	Q7Q0S7	anopheles g
120	135	6.4	2013	2	Q8VHZ8	rattus norv
121	135	6.4	298	2	Q9BRC8	mus musculu
122	134.5	6.4	303	2	Q8CE95	mus musculu
123	134.5	6.4	2597	2	Q7ZXR4	xenopus lae
124	134.5	6.4	442	2	Q6WRH9	rattus norv
125	134	6.4	1946	2	Q9BY67	homo sapien
126	134	6.4	2217	2	Q68J72	apis mellif
127	134	6.4	2623	2	Q8AV57	gallus gall
128	134	6.4	310	2	Q6WRI0	homo sapien
129	133.5	6.4	321	2	Q68FQ2	rattus norv
130	133.5	6.4	434	2	Q6INF0	xenopus lae
131	133.5	6.4	484	2	Q6DN72	homo sapien
132	133.5	6.4	532	2	Q26475	schistocerc
133	133.5	6.4	532	2	Q6NNU3	drosophila
134	133.5	6.4	532	2	Q9VLF0	drosophila
135	133.5	6.4	1164	2	Q66MN5	drosophila
136	133.5	6.4	5175	2	Q81OL3	caenorhabdi
137	133.5	6.4	5198	2	O76518	caenorhabdi
138	133	6.3	285	2	Q8VE93	mus musculu
139	133	6.3	349	1	LACH_SCHAM	schistocerc
140	133	6.3	948	2	Q9VME2	drosophila
141	133	6.3	1730	2	Q26474	schistocerc
142	132.5	6.3	298	2	Q7YRQ7	sus scrofa
143	132.5	6.3	641	2	Q91IS9	ciona intes
144	132.5	6.3	765	2	Q86SD2	m vascular
145	132.5	6.3	765	2	Q9BKQ1	aplysia cal
146	132.5	6.3	812	2	Q9TWA4	aplysia cal
147	132.5	6.3	812	2	Q9BKQ0	aplysia cal
148	132.5	6.3	932	2	Q9TWA5	aplysia cal
149	132.5	6.3	932	2	Q9BKP9	aplysia cal
150	132.5	6.3	1065	1	LIG2_HUMAN	homo sapien
151	132.5	6.3	1369	1	NFAS_CHICK	gallus gall
152	132.5	6.3	296	2	Q9TWA6	aplysia cal
153	132	6.3	300	2	O640C0	gallus gall
154	132	6.3	394	2	O7SYQ7	xenopus lae
155	132	6.3	464	2	Q6AYD4	rattus norv
156	132	6.3	1746	2	Q6GL25	xenopus tro
157	132	6.3	2012	1	DSCA_HUMAN	homo sapien
158	131.5	6.3	433	2	Q8WY19	homo sapien
159	131.5	6.3	433	2	Q9V644	drosophila
160	131.5	6.3	1247	1	SIL7_HUMAN	homo sapien
161	131.5	6.3	2673	2	Q9Y286	homo sapien
162	131	6.3	259	2	O70QS6	anopheles g
163	131	6.2	285	2	Q96SC3	homo sapien
164	131	6.2	309	2	Q9YSB2	homo sapien
165	131	6.2	1073	2	Q8BTK0	mus musculu
166	131	6.2	1173	2	Q91YV7	mus musculu
167	131	6.2	4391	1	PGBM_HUMAN	drosophila
168	130.5	6.2	272	2	Q6NR54	mus musculu
169	130.5	6.2	456	2	O70356	mus musculu
170	130.5	6.2	702	2	Q8R5M8	mus musculu
171	130	6.2	253	2	Q69ZY8	mus musculu
172	130	6.2	316	2	Q9D8H2	mus musculu
173	130	6.2	445	2	Q9D8H2	mus musculu
174	130	6.2	515	2	Q8VE98	mus musculu
175	130	6.2	540	1	PVR1_PIG	sus scrofa
176	130	6.2	582	2	Q8N0Z9	homo sapien
177	130	6.2	915	2	Q8R4B3	mus musculu

No.	Score		Length	N	Name	Accession	Organism
178	130	6.2	955	1	MDG1_HUMAN	Q8NFP4	homo sapien
179	129.5	6.2	300	2	Q68SF0	Q68SP0	mus musculu
180	129.5	6.2	1040	1	AXO1_RAT	P22003	rattus norv
181	129.5	6.2	3375	1	UN52_CAEEL	Q05661	caenorhabdi
182	129.5	6.2	6658	2	O76281	O76281	drosophila
183	129.5	6.2	8647	2	Q7KQP5	Q7KQP5	drosophila
184	129.5	6.2	8648	2	Q7KQP6	Q7KQP6	drosophila
185	129.5	6.2	8930	2	Q7KQP7	Q7KQP7	drosophila
186	129.5	6.2	8943	2	Q9V4F7	Q9V4F7	drosophila
187	129	6.1	208	2	Q80WN3	Q80WN3	mus musculu
188	129	6.1	295	2	Q9QYL6	Q9QYL6	mus musculu
189	129	6.1	295	2	Q92ZH8	Q92ZH8	mus musculu
190	129	6.1	309	2	Q7TMH2	Q7TMH2	mus musculu
191	129	6.1	314	2	Q8R4Y0	Q8R4Y0	mus musculu
192	129	6.1	324	2	Q64381	Q64381	mus musculu
193	129	6.1	343	2	Q8R4L1	Q8R4L1	mus musculu
194	129	6.1	356	2	Q91562	Q91562	mus musculu
195	129	6.1	445	1	KMLS_CHICK	P11799	gallus gall
196	129	6.1	1427	2	Q9QYL4	Q9QYL4	mus musculu
197	129	6.1	1906	2	Q6PF50	Q6PF50	xenopus lae
198	128.5	6.1	306	1	AXO1_MOUSE	Q61330	mus musculu
199	128.5	6.1	775	2	Q8T172	Q8T172	methanosarc
200	128.5	6.1	1040	2	Q8IZY4	Q8IZY4	mus musculu
201	128.5	6.1	1386	2	Q9VQ64	Q9VQ64	drosophila
202	128.5	6.1	2053	2	Q8R202	Q8R202	mus musculu
203	128	6.1	255	2	Q9D7L8	Q9D7L8	mus musculu
204	128	6.1	257	2	Q8BYS4	Q8BYS4	mus musculu
205	128	6.1	261	2	Q8BIN0	Q8BIN0	mus musculu
206	128	6.1	343	2	Q7PSN2	Q7PSN2	anopheles g
207	128	6.1	386	2	Q96RD9	Q96RD9	homo sapien
208	128	6.1	392	2	Q6RD9	Q6RD9	anopheles g
209	128	6.1	977	2	Q7PGG9	Q7PGG9	homo sapien
210	128	6.1	2133	2	Q7Q8F3	Q7Q8F3	mus musculu
211	128	6.1	299	2	Q8WXU7	Q8WXU7	anopheles g
212	128	6.1	442	2	Q7PPH8	Q7PPH8	homo sapien
213	127.5	6.1	1028	2	Q8CD84	Q8CD84	brachydanio
214	127.5	6.1	1340	2	Q76MU9	Q76MU9	anopheles g
215	127.5	6.1	1496	2	Q8NDA2	Q8NDA2	homo sapien
216	127	6.1	282	2	Q8VIM1	Q8VIM1	homo sapien
217	127	6.1	282	2	Q7TPU2	Q7TPU2	homo sapien
218	127	6.1	337	1	OPCM_CHICK	Q9DF61	gallus gall
219	127	6.1	344	2	Q9DF61	Q9DF61	gallus gall
220	127	6.1	725	1	SIL8_HUMAN	SIL8_HUMAN	homo sapien
221	127	6.1	1115	2	Q8N6I2	Q8N6I2	mus musculu
222	127	6.1	1249	1	NCA2_MOUSE	NCA2_MOUSE	pan troglod
223	127	6.1	1555	1	NCA1_MOUSE	NCA1_MOUSE	mus musculu
224	127	6.1	2053	2	Q90Z04	Q90Z04	xenopus lae
225	127	6.1	2092	2	Q7PPH8	Q7PPH8	anopheles g
226	127	6.1	2113	2	Q8WXU7	Q8WXU7	homo sapien
227	126.5	6.1	318	2	Q76MU9	Q76MU9	brachydanio
228	126.5	6.0	433	2	Q8TD84	Q8TD84	xenopus lae
229	126.5	6.0	499	1	Q91664	Q91664	xenopus tro
230	126.5	6.0	597	2	Q6DJ83	Q6DJ83	homo sapien
231	126.5	6.0	812	1	SILL_PANTR	SILL_PANTR	pan troglod
232	126.5	6.0	865	2	Q68DA2	Q68DA2	homo sapien
233	126.5	6.0	924	2	Q6DG17	Q6DG17	homo sapien
234	126.5	6.0	924	2	Q90203	Q90203	homo sapien
235	126.5	6.0	986	1	ICA5_HUMAN	ICA5_HUMAN	homo sapien
236	126.5	6.0	1056	2	Q66MN4	Q66MN4	petromyzon
237	126	6.0	378	2	Q90203	Q90203	xenopus lae
238	126	6.0	413	2	Q7QBV2	Q7QBV2	anopheles g
239	126	6.0	463	2	Q8HYV1	Q8HYV1	homo sapien
240	126	6.0	885	2	Q8HYV2	Q8HYV2	sus scrofa
241	126	6.0	886	1	SIL9_HUMAN	SIL9_HUMAN	homo sapien
242	126	6.0	947	1	MUSK_CHICK	MUSK_CHICK	gallus gall
243	126	6.0	1476	2	Q7Q029	Q7Q029	anopheles g
244	125.5	6.0	303	2	Q7Q154	Q7Q154	anopheles g
245	125.5	6.0	336	2	Q46551	Q46551	anopheles g
246	125.5	6.0	412	2	Q9R1E1	Q9R1E1	hylobates s
247	125.5	6.0	476	2	Q9R1E1	Q9R1E1	rattus norv
248	125.5	6.0	499	2	Q6AYP5	Q6AYP5	homo sapien
249	125.5	6.0	626	2	O7Z728	O7Z728	xenopus lae
250	125.5	6.0	707	2	Q6DCH3	Q7PWJ1	anopheles g

#					accession	organism
251	125.5	6.0	1443	2	Q8MTB2	drosophila
252	125.5	6.0	1765	2	Q9V830	drosophila
253	125.5	6.0	1770	2	Q9VS29	drosophila
254	125	6.0	311	2	Q6DN73	homo sapien
255	125	6.0	313	2	O57596	gallus gall
256	125	6.0	315	2	Q9DGI5	gallus gall
257	125	6.0	439	2	Q6GTU4	homo sapien
258	125	6.0	467	2	Q91VT9	mus musculu
259	125	6.0	510	2	Q91NY8	homo sapien
260	125	6.0	538	2	Q9NWQ7	homo sapien
261	125	6.0	1006	2	Q61DE9	drosophila
262	125	6.0	18412	2	Q7ZZ61	brachydanio
263	125	5.9	259	2	Q7ZZQ1	homo sapien
264	124.5	5.9	344	2	O93242	gallus gall
265	124.5	5.9	353	1	CEPU_CHICK	gallus gall
266	124.5	5.9	387	2	Q86XK7	homo sapien
267	124.5	5.9	412	2	Q6MZS4	homo sapien
268	124.5	5.9	815	2	Q80SB9	brachydanio
269	124.5	5.9	848	1	P13591	homo sapien
270	124.5	5.9	877	2	NCA1_HUMAN	homo sapien
271	124	5.9	394	2	Q9G8H3	halocynthia
272	124	5.9	623	2	Q6DCI6	homo sapien
273	124	5.9	688	2	Q8BY18	xenopus lae
274	124	5.9	697	2	Q80ZE3	mus musculu
275	124	5.9	853	1	Q7PMJ7	anopheles g
276	124	5.9	1011	2	NCA1_BOVIN	bos taurus
277	124	5.9	1240	1	NPAS_HUMAN	homo sapien
278	124	5.9	1240	1	NPAS_MOUSE	mus musculu
279	124	5.9	1251	2	O81OU3	mus musculu
280	124	5.9	1251	2	P97685	rattus norv
281	124	5.9	1366	1	ROB3_MOUSE	mus musculu
282	123.5	5.9	336	1	C226_HUMAN	homo sapien
283	123.5	5.9	338	1	Q15762	homo sapien
284	123.5	5.9	350	2	LAMP_CHICK	gallus gall
285	123.5	5.9	383	2	O02869	gallus gall
286	123.5	5.9	412	2	Q75Ml9	homo sapien
287	123.5	5.9	454	1	O63611	rattus norv
288	123.5	5.9	521	2	CEA1_MOUSE	mus musculu
289	123.5	5.9	521	1	Q92SP3	mus musculu
290	123.5	5.9	538	1	SILL_HUMAN	sus scrofa
291	123.5	5.9	595	1	Q96PQl	homo sapien
292	123.5	5.9	605	2	Q921P2	mus musculu
293	123.5	5.9	800	1	Q918X3	brachydanio
294	123.5	5.9	838	2	Q8BQ96	mus musculu
295	123.5	5.9	838	2	Q8C4B2	mus musculu
296	123.5	5.9	875	2	Q91ZY7	mus musculu
297	123.5	5.9	1091	2	NCA1_CHICK	gallus gall
298	123.5	5.9	1151	2	Q9QVN5	rattus norv
299	123.5	5.9	1256	1	NRCA_MOUSE	mus musculu
300	123.5	5.9	1723	2	Q8I0U4	mus musculu
301	123	5.9	1842	2	Q8IZY3	homo sapien
302	123	5.9	265	2	Q9NGZ0	homo sapien
303	123	5.9	304	1	Q9BPN5	caenorhabdi
304	123	5.9	344	1	NTRI_HUMAN	homo sapien
305	123	5.9	373	2	Q7KYP5	homo sapien
306	123	5.9	464	2	O16170	homo sapien
307	123	5.9	467	2	O8C6F2	homo sapien
308	123	5.9	468	2	Q96CA7	homo sapien
309	123	5.9	526	1	CEA1_HUMAN	homo sapien
310	123	5.9	779	2	O97136	homo sapien
311	123	5.9	837	2	O97137	manduca sex
312	123	5.9	1694	2	SN_MOUSE	mus musculu
313	122.5	5.8	400	2	Q8HY16	cebus apell
314	122.5	5.8	738	1	PEC1_HUMAN	homo sapien
315	122.5	5.8	761	1	NCA2_HUMAN	homo sapien
316	122.5	5.8	1032	2	O8UVD6	brachydanio
317	122.5	5.8	1284	2	NRCA_CHICK	gallus gall
318	122.5	5.8	1419	2	Q98SW3	brachydanio
319	122	5.8	240	2	O6MG96	rattus norv
320	122	5.8	410	2	O6R3M2	bombyx mori
321	122	5.8	1036	1	P28685	gallus gall
322	122	5.8	1166	2	AXO1_CHICK	gallus gall
323	121.5	5.8	244	2	Q95T89	drosophila

#					accession	organism	accession	organism
324	121.5	5.8	320	2	Q7QOP8	anopheles g	Q7QOP8	anopheles g
325	121.5	5.8	337	2	P97268	cavia porce	P97268	cavia porce
326	121.5	5.8	344	2	CEA6_HUMAN	homo sapien	CEA6_HUMAN	homo sapien
327	121.5	5.8	508	2	P40199	homo sapien	P40199	homo sapien
328	121.5	5.8	508	2	Q8CED8	mus musculu	Q8CED8	mus musculu
329	121.5	5.8	549	2	Q8R007	homo sapien	Q8R007	homo sapien
330	121.5	5.8	595	2	Q9NQS3	homo sapien	Q9NQS3	homo sapien
331	121.5	5.8	1154	2	Q62RS5	homo sapien	Q62RS5	homo sapien
332	121.5	5.8	1180	2	Q9QVN3	rattus sp.	Q9QVN3	rattus sp.
333	121.5	5.8	1194	2	Q8T157	methanobarc	Q8T157	methanosarc
334	121.5	5.8	1197	2	Q8T157	homo sapien	Q8T157	homo sapien
335	121.5	5.8	1198	2	Q6PW38	rattus norv	Q6PW38	rattus norv
336	121.5	5.8	1206	2	Q6PW36	rattus norv	Q6PW36	rattus norv
337	121.5	5.8	1206	2	Q6PW37	rattus norv	Q6PW37	rattus norv
338	121.5	5.8	1209	2	Q6PW39	rattus norv	Q6PW39	rattus norv
339	121.5	5.8	1214	2	NRCA_RAT	rattus norv	NRCA_RAT	rattus norv
340	121.5	5.8	1224	1	P97686	rattus norv	P97686	rattus norv
341	121.5	5.8	1299	2	Q6NV23	homo sapien	Q6NV23	homo sapien
342	121	5.8	366	2	Q66KX2	xenopus lae	Q66KX2	xenopus lae
343	121	5.8	390	2	Q7YZA7	drosophila	Q7YZA7	drosophila
344	121	5.8	410	2	P91670	drosophila	P91670	drosophila
345	121	5.8	528	2	Q28939	sus scrofa	Q28939	sus scrofa
346	121	5.8	538	2	O18466	hirudo medi	O18466	hirudo medi
347	121	5.8	858	2	O90YM2	brachydanio	O90YM2	brachydanio
348	121	5.8	1031	2	Q7Q3K8	anopheles g	Q7Q3K8	anopheles g
349	121	5.8	1086	2	Q7QH02	anopheles g	Q7QH02	anopheles g
350	121	5.8	1155	1	NRCA_HUMAN	homo sapien	NRCA_HUMAN	homo sapien
351	121	5.8	1304	1	Q92823	homo sapien	Q92823	homo sapien
352	120.5	5.8	163	2	Q8K1H8	mus musculu	Q8K1H8	mus musculu
353	120.5	5.8	202	2	Q6NTA1	homo sapien	Q6NTA1	homo sapien
354	120.5	5.8	265	2	O7PUU3	brachydanio	O7PUU3	brachydanio
355	120.5	5.8	358	1	O90490	homo sapien	O90490	homo sapien
356	120.5	5.8	410	2	SIL6_HUMAN	homo sapien	SIL6_HUMAN	homo sapien
357	120.5	5.8	442	1	Q9UEI6	homo sapien	Q9UEI6	homo sapien
358	120.5	5.8	449	2	Q1V87	mus musculu	Q1V87	mus musculu
359	120.5	5.8	529	2	Q9JLB9	homo sapien	Q9JLB9	homo sapien
360	120.5	5.7	549	2	Q6PDN3	mus musculu	Q6PDN3	mus musculu
361	120.5	5.7	312	2	Q9BXR1	homo sapien	Q9BXR1	homo sapien
362	120	5.7	333	2	AMAL_DROME	drosophila	AMAL_DROME	drosophila
363	120	5.7	341	2	Q7KSX2	drosophila	Q7KSX2	drosophila
364	120	5.7	410	2	Q6R3L9	bombyx mand	Q6R3L9	bombyx mand
365	120	5.7	483	2	Q9DBP8	mus musculu	Q9DBP8	mus musculu
366	120	5.7	510	2	Q96K15	mus musculu	Q96K15	mus musculu
367	120	5.7	662	2	Q8MJZ6	pan troglod	Q8MJZ6	pan troglod
368	120	5.7	1093	2	LIG1_HUMAN	homo sapien	LIG1_HUMAN	homo sapien
369	119.5	5.7	298	2	JAM2_HUMAN	homo sapien	JAM2_HUMAN	homo sapien
370	119.5	5.7	298	2	Q6YNC1	homo sapien	Q6YNC1	homo sapien
371	119.5	5.7	450	2	Q9VR25	drosophila	Q9VR25	drosophila
372	119.5	5.7	520	2	Q925P2	drosophila	Q925P2	drosophila
373	119.5	5.7	529	2	Q7TQM3	mus musculu	Q7TQM3	mus musculu
374	119.5	5.7	547	1	CD19_MOUSE	mus musculu	CD19_MOUSE	mus musculu
375	119.5	5.7	549	2	Q9DD06	mus musculu	Q9DD06	mus musculu
376	119.5	5.7	672	2	Q8IP70	drosophila	Q8IP70	drosophila
377	119.5	5.7	725	2	O73634	homo sapien	O73634	homo sapien
378	119.5	5.7	858	2	O86X47	homo sapien	O86X47	homo sapien
379	119.5	5.7	917	1	ICA5_MOUSE	mus musculu	ICA5_MOUSE	mus musculu
380	119.5	5.7	1643	2	O7QGT8	anopheles g	O7QGT8	anopheles g
381	119	5.7	1950	2	O80YN8	mus musculu	O80YN8	mus musculu
382	119	5.7	334	2	O02870	homo sapien	O02870	homo sapien
383	119	5.7	391	2	O7QJG1	anopheles g	O7QJG1	anopheles g
384	119	5.7	410	2	Q6R3M0	bombyx mori	Q6R3M0	bombyx mori
385	119	5.7	410	2	Q6RKB2	rattus norv	Q6RKB2	rattus norv
386	119	5.7	727	2	Q8NI15	homo sapien	Q8NI15	homo sapien
387	119	5.7	769	1	FGR3_HUMAN	homo sapien	FGR3_HUMAN	homo sapien
388	119	5.7	806	1	P22607	homo sapien	P22607	homo sapien
389	119	5.7	837	2	Q6RKB3	rattus norv	Q6RKB3	rattus norv
390	119	5.7	907	2	Q9NEGO	drosophila	Q9NEGO	drosophila
391	119	5.7	1091	2	LIG1_MOUSE	mus musculu	LIG1_MOUSE	mus musculu
392	119	5.7	1994	2	Q6ZPP2	mus musculu	Q6ZPP2	mus musculu
393	119	5.7	2176	2	Q6V4S5	mus musculu	Q6V4S5	mus musculu
394	119	5.7	4179	2	Q9W4Y4	drosophila	Q9W4Y4	drosophila
395	119	5.7	9270	2	Q8MLD9	drosophila	Q8MLD9	drosophila
396	119	5.7	26926	2	Q10466	homo sapien	Q10466	homo sapien

No					ID	Accession	Organism
397	119	5.7	26926	2	Q8WZB3	Q8wzb3	homo sapien
398	118.5	5.6	152	2	Q8BSQ8	Q8bsq8	mus musculu
399	118.5	5.6	262	2	Q6UX20	Q6ux20	homo sapien
400	118.5	5.6	413	2	Q70BV1	Q70bv1	homo sapien
401	118.5	5.6	458	2	Q7GBV1	Q7gbv1	anopheles g
402	118.5	5.6	462	2	Q63093	Q63093	rattus norv
403	118.5	5.6	519	1	Q7RTW1	Q7rtw1	homo sapien
404	118.5	5.6	640	2	ECTO_RAT	P16573	rattus norv
405	118.5	5.6	1561	2	Q92402	Q92d2	homo sapien
406	118.5	5.6	163	2	Q9NVU5	Q9nvu5	homo sapien
407	118	5.6	289	2	Q9QYL5	Q9qyl5	mus musculu
408	118	5.6	344	1	NTRI_MOUSE	Q99pj0	mus musculu
409	118	5.6	344	2	Q8BG33	Q8bg33	m mus muscu
410	118	5.6	359	2	Q7ZX17	Q7zx17	xenopus lae
411	118	5.6	413	2	Q9VAR6	Q9var6	drosophila
412	118	5.6	501	2	Q6Q147	Q6q147	bos taurus
413	118	5.6	547	2	ICA3_HUMAN	P32942	homo sapien
414	118	5.6	547	2	Q6PD68	Q6pd68	homo sapien
415	118	5.6	782	2	Q61563	Q61563	mus musculu
416	118	5.6	807	2	Q9ESA5	Q9esa5	rattus norv
417	118	5.6	807	2	Q6NY23	Q6ny23	brachydanio
418	118	5.6	837	2	NCM2_MOUSE	O35136	mus musculu
419	118	5.6	1103	2	O6QNF3	O6qnf3	canis famil
420	118	5.6	1338	1	VGR1_HUMAN	P17948	h vascular
421	118	5.6	4824	1	Q95YM1	Q95ym1	procambarus
422	118	5.6	17352	2	Q95YM2	Q95ym2	procambarus
423	117.5	5.6	338	1	LAMP_HUMAN	Q13449	homo sapien
424	117.5	5.6	340	2	Q9W3N2	Q9w3n2	drosophila
425	117.5	5.6	344	2	Q13774	Q13774	homo sapien
426	117.5	5.6	509	2	Q92OC2	Q92oc2	mus musculu
427	117.5	5.6	533	2	Q8NCB6	Q8ncb6	homo sapien
428	117.5	5.6	1028	2	P97528	P97528	rattus norv
429	117.5	5.6	1056	2	Q7ZW34	Q7zw34	brachydanio
430	117.5	5.6	1092	1	P36335	P36335	xenopus lae
431	117.5	5.6	1302	1	NRG_DROME	P20241	drosophila
432	117.5	5.6	1389	2	Q90Z69	Q90z69	brachydanio
433	117.5	5.6	2008	2	Q9VEJ5	Q9vej5	drosophila
434	117.5	5.6	2046	2	Q7KSE9	Q7kse9	drosophila
435	117.5	5.6	8625	2	Q8GD06	Q8gd06	procambarus
436	117	5.6	351	2	Q6WEB2	Q6web2	branchiosto
437	117	5.6	401	2	Q7PSS8	Q7pss8	anopheles g
438	117	5.6	448	2	Q9JHL7	Q9jhl7	rattus norv
439	117	5.6	459	2	Q9JHL6	Q9jhl6	rattus norv
440	117	5.6	484	2	Q6BE00	Q6be00	xenopus lae
441	117	5.6	650	1	LIB1_HUMAN	Q8nhl6	h leukocyte
442	117	5.6	739	1	VCA1_RAT	Q9534	rattus norv
443	117	5.6	858	1	NCA1_RAT	P13596	rattus norv
444	117	5.6	1062	2	Q8BKG3	Q8bkg3	mus musculu
445	117	5.6	1445	2	Q63155	Q63155	rattus norv
446	117	5.6	2164	2	DCC_HUMAN	P43146	homo sapien
447	117	5.6	285	2	Q9IAR9	Q9iar9	gallus gall
448	116.5	5.6	316	2	Q7PNI4	Q7pni4	anopheles g
449	116.5	5.6	316	1	Q8WPB3	Q8wpb3	drosophila
450	116.5	5.6	338	1	LAMP_RAT	Q62813	rattus norv
451	116.5	5.6	341	1	LAMP_MOUSE	Q8blk3	mus musculu
452	116.5	5.6	421	2	Q7PV30	Q7pv30	anopheles g
453	116.5	5.6	474	2	Q7PKE3	Q7pke3	anopheles g
454	116.5	5.6	554	2	Q9W4R3	Q9w4r3	drosophila
455	116.5	5.6	620	2	Q6IGL3	Q6igl3	drosophila
456	116.5	5.6	806	1	CEK2_CHICK	P18460	gallus gall
457	116.5	5.6	899	2	Q7PQM9	Q7pqm9	anopheles g
458	116.5	5.6	972	2	Q26614	Q26614	strongyloce
459	116.5	5.6	1040	1	AXO1_HUMAN	Q02246	homo sapien
460	116.5	5.6	1051	1	PTK7_CHICK	Q91048	gallus gall
461	116.5	5.6	1598	2	Q92PI4	Q9p214	homo sapien
462	116	5.6	237	2	Q6DQX5	Q6dqx5	oryctolagus
463	116	5.6	316	2	Q6UXI2	Q6uxi2	homo sapien
464	116	5.6	333	1	C226_MOUSE	Q84f0	mus musculu
465	116	5.6	344	1	NTRI_RAT	Q62718	rattus norv
466	116	5.6	344	2	Q6B0I4	Q6b0i4	rattus norv
467	116	5.6	435	2	Q8N3J6	Q8n3j6	homo sapien
468	116	5.5	1027	2	Q90W79	Q90w79	gallus gall
469	116	5.5	1189	2	Q9P2J2	Q9p2j2	homo sapien
470	116	5.5	1447	1	DCC_MOUSE	P70211	mus musculu
471	116	5.5	1709	1	SN_HUMAN	Q9bzz2	homo sapien
472	115.5	5.5	390	1	Q6P500	Q6p500	rattus norv
473	115.5	5.5	421	2	Q7QLK4	Q7qlk4	anopheles g
474	115.5	5.5	437	2	Q81ZP8	Q81zp8	homo sapien
475	115.5	5.5	485	1	PODX_RAT	Q9wcg2	rattus norv
476	115.5	5.5	527	2	Q9ERF7	Q9erf7	cricetulus
477	115.5	5.5	590	2	Q6P4T5	Q6p4t5	mus musculu
478	115.5	5.5	725	2	O73633	O73633	xenopus lae
479	115.5	5.5	731	2	Q8SPI6	Q8spi6	macropus eu
480	115.5	5.5	828	2	Q9DGK3	Q9dgk3	xenopus lae
481	115.5	5.5	1252	2	Q96DN3	Q96dn3	homo sapien
482	115.5	5.5	1252	2	Q7Z2Z9	Q7z2z9	homo sapien
483	115.5	5.5	1255	2	Q7YQL8	Q7yql8	pan troglod
484	115.5	5.5	1257	1	CAML_HUMAN	P32004	homo sapien
485	115.5	5.5	1493	1	NEO1_MOUSE	P97798	mus musculu
486	115	5.5	237	2	Q9N2P7	Q9n2p7	drosophila
487	115	5.5	294	2	Q9NL88	Q9nl88	drosophila
488	115	5.5	399	2	Q9NL88	Q9nl88	drosophila
489	115	5.5	424	2	Q9W0S5	Q9w0s5	drosophila
490	115	5.5	510	2	Q9NFS3	Q9nfs3	drosophila
491	115	5.5	602	2	Q86Y29	Q86y29	homo sapien
492	115	5.5	650	2	Q8NA84	Q8na84	homo sapien
493	115	5.5	837	2	Q7Z7F2	Q7z7f2	homo sapien
494	115	5.5	1109	2	Q7ZF3	Q7z7f3	homo sapien
495	115	5.5	1125	2	Q6PSH3	Q6psh3	mus musculu
496	115	5.5	1209	2	Q7QEC1	Q7qec1	homo sapien
497	115	5.5	1302	1	P70232	P70232	anopheles g
498	115	5.5	2403	2	VGR2_BRARE	O18906	brachydanio
499	115	5.5	7210	2	Q8MLD5	Q8mld5	drosophila
500	115	5.5	217	2	C226_MACMU	Q6gm08	macaca mula
501	115.5	5.5	294	2	Q6GM08	Q6nv41	xenopus lae
502	115	5.5	345	2	Q6NV41	Q8hy14	brachydanio
503	115	5.5	363	2	Q8HY14	Q61351	oryctolagus
504	115	5.5	412	2	Q61351	Q61351	mus musculu
505	115	5.5	458	2	Q61351	Q7pgl7	anopheles g
506	115	5.5	489	2	Q7PGL7	Q9bxn7	homo sapien
507	114.5	5.5	497	2	Q9BXN7	Q8n441	homo sapien
508	114.5	5.5	504	2	Q8N441	Q9had7	homo sapien
509	114.5	5.5	517	1	Q9HAD7	Q15223	mus musculu
510	114.5	5.5	521	1	PVR1_HUMAN	P61352	homo sapien
511	114.5	5.5	517	2	Q61352	Q7pzs8	mus musculu
512	114.5	5.5	551	2	Q7PZS8	P32507	anopheles g
513	114.5	5.5	530	2	PVR2_MOUSE	Q66iv0	mus musculu
514	114.5	5.5	530	2	Q66IV0	Q9w4t9	xenopus lae
515	114.5	5.5	538	2	Q8MSN7	Q9n9y9	drosophila
516	114.5	5.5	551	2	Q9W4T9	Q97174	drosophila
517	114.5	5.5	517	1	Q9N9Y9	P16170	anopheles g
518	114.5	5.5	719	2	Q97174	Q94155	drosophila
519	114.5	5.5	956	2	NCA1_XENLA	Q8wz53	xenopus lae
520	114.5	5.5	959	2	Q94155	Q75296	drosophila
521	114.5	5.5	975	1	Q8WZ53	Q9bdm2	caenorhabdi
522	114.5	5.5	1088	1	Q75296	Q6dfy2	homo sapien
523	114.5	5.5	1415	2	Q9BDM2	Q9bdm2	homo sapien
524	114.5	5.5	5604	2	Q6DFY2	O08835	homo sapien
525	114.5	5.5	2235	2	Q9BDM2	O08835	homo sapien
526	114.5	5.5	323	2	O08835	Q9jlb7	mus musculu
527	114.5	5.5	337	2	O08835	Q8hy15	cercopithec
528	114.5	5.4	401	2	Q9JLB7	O08835	mus musculu
529	114.5	5.4	403	2	Q8HY15	Q9jlb7	cercopithec
530	114	5.4	438	2	O08835	ICA_BOVIN	lemur catta
531	114	5.4	544	2	Q9JLB7	Q9vct4	mus musculu
532	114	5.4	337	2	ICA_BOVIN	O59199	homo sapien
533	114	5.4	323	2	Q9VCT4	Q8mjz5	homo sapien
534	114	5.4	403	2	NRG1_CHICK	P01832	bos taurus
535	114	5.4	544	1	Q8MJZ5	O90ym0	drosophila
536	114	5.4	545	2	O59199	Q8c6x1	gallus gall
537	114	5.4	602	2	Q9VCT4	Q9vct4	drosophila
538	114	5.4	645	2	Q8MJZ5	Q8mjz5	pan troglod
539	114	5.4	773	2	PIGR_RABBIT	P01832	oryctolagus
540	114	5.4	795	2	O90YM0	O90ym0	brachydanio
541	114	5.4	1028	2	Q8C6X1	Q8c6x1	mus musculu

No.	V1	V2	Len	T	ID	Accession	Organism
543	114	5.4	1028	2	Q9JMB8	Q9jmb8	mus musculu
544	114	5.4	1045	2	Q86C37	Q86c37	MUSK_HUMAN
545	114	5.4	1073	2	Q9TX18	Q9tx18	caenorhabdi
546	114	5.4	1097	1	PGDR_RAT	O50030	rattus norv
547	114	5.4	1177	2	Q6GQB1	Q6gqb1	xenopus lae
548	114	5.4	1320	2	Q96KF5	Q96kf5	homo sapien
549	114	5.4	1320	2	Q86TC9	Q86tc9	homo sapien
550	114	5.4	1735	2	Q7Q916	Q7q916	drosophila
551	113.5	5.4	232	2	Q7PJ18	Q7pj18	anopheles g
552	113.5	5.4	284	2	Q9NX42	Q9nx42	homo sapien
553	113.5	5.4	296	2	Q6PJ56	Q6pj56	homo sapien
554	113.5	5.4	316	2	Q8WP94	Q8wp94	drosophila
555	113.5	5.4	327	2	Q96IQ7	Q96iq7	homo sapien
556	113.5	5.4	382	2	Q7PSH7	Q7psh7	anopheles g
557	113.5	5.4	388	2	Q8NC34	Q8nc34	homo sapien
558	113.5	5.4	417	1	PVR_CERAE	P32506	cercopithec
559	113.5	5.4	534	2	Q98W4	Q98w4	homo sapien
560	113.5	5.4	754	2	Q8NB18	Q8nb18	homo sapien
561	113.5	5.4	771	2	Q7QEY8	Q7qey8	anopheles g
562	113.5	5.4	939	2	Q967X6	Q967x6	drosophila
563	113.5	5.4	939	2	Q9VB35	Q9vb35	drosophila
564	113.5	5.4	1248	2	Q9XT41	Q9xt41	cercopithec
565	113.5	5.4	1255	2	Q7YQL7	Q7yql7	pongo pygma
566	113.5	5.4	1386	1	ROB3_HUMAN	Q96ME0	homo sapien
567	113.5	5.4	1614	2	Q8UVD7	Q8uvd7	brachydanio
568	113.5	5.4	1675	2	Q98W4	Q98w4	xenopus lae
569	113	5.4	340	2	Q7Q807	Q7q807	anopheles g
570	113	5.4	430	2	Q8N4F1	Q8n4f1	homo sapien
571	113	5.4	430	2	Q7QG58	Q7qg58	anopheles g
572	113	5.4	636	2	Q22040	Q22040	caenorhabdi
573	113	5.4	816	2	Q91285	Q91285	pleurodeles
574	113	5.4	1277	1	CAML_FUGRU	Q98902	fugu rubrip
575	113	5.4	3100	2	Q7KYN5	Q7kyn5	homo sapien
576	113	5.4	4650	2	Q15598	Q15598	homo sapien
577	112.5	5.4	226	2	Q7PYG1	Q7pyg1	anopheles g
578	112.5	5.4	338	2	Q7Z3W6	Q7z3w6	homo sapien
579	112.5	5.4	345	1	OPCM_HUMAN	Q14982	homo sapien
580	112.5	5.4	362	2	Q9JHQ1	Q9jhq1	rattus norv
581	112.5	5.4	363	2	O46147	O46147	onchocerca
582	112.5	5.4	437	2	Q8NF56	Q8nf56	homo sapien
583	112.5	5.4	440	2	Q6ZMD4	Q6zmd4	homo sapien
584	112.5	5.4	639	1	NRG1_HUMAN	Q02297	homo sapien
585	112.5	5.4	743	2	Q8R6B2	Q8r6b2	vibriophage
586	112.5	5.4	1259	1	CAML_RAT	Q05695	rattus norv
587	112.5	5.4	1259	2	Q6PGJ3	Q6pgj3	mus musculu
588	112.5	5.4	1342	2	Q9GPP6	Q9gpp6	drosophila
589	112.5	5.4	1342	2	Q9VPZ7	Q9vpz7	drosophila
590	112.5	5.4	2029	1	LAR_DROME	P16621	drosophila
591	112.5	5.4	2029	2	Q9VIS8	Q9vis8	drosophila
592	112.5	5.4	2224	2	Q9U1M1	Q9u1m1	drosophila
593	112	5.4	352	1	NEGR_HUMAN	Q7Z3B1	homo sapien
594	112	5.4	387	2	Q64JA4	Q64ja4	pan troglod
595	112	5.4	829	2	Q9PSV8	Q9psv8	xenopus lae
596	112	5.4	913	2	Q8T3E5	Q8t3e5	caenorhabdi
597	112	5.4	928	2	Q19128	Q19128	caenorhabdi
598	112	5.4	946	2	Q07153	Q07153	torpedo cal
599	112	5.4	955	2	Q8MQ86	Q8mq86	caenorhabdi
600	112	5.4	1066	2	Q8MSR5	Q8msr5	drosophila
601	112	5.4	1070	1	PTK7_HUMAN	Q13308	homo sapien
602	112	5.4	1212	2	Q9STG0	Q9stg0	drosophila
603	112	5.4	1269	2	O01632	O01632	caenorhabdi
604	112	5.4	1273	2	O44928	O44928	caenorhabdi
605	112	5.4	1530	2	Q8Y479	Q8y479	listeria mo
606	112	5.4	3215	2	Q8IRV7	Q8irv7	drosophila
607	112	5.4	4117	2	Q8IRV9	Q8irv9	drosophila
608	112	5.4	4223	2	Q8MPN3	Q8mpn3	drosophila
609	112	5.4	4228	2	Q8IRV8	Q8irv8	drosophila
610	112	5.4	7105	2	Q7PXW9	Q7pxw9	anopheles g
611	111.5	5.3	267	2	Q8NC05	Q8nc05	homo sapien
612	111.5	5.3	390	2	Q95KI3	Q95ki3	macaca fasc
613	111.5	5.3	400	1	HPL4_MOUSE	Q80WM4	mus musculu
614	111.5	5.3	443	2	Q8N2F4	Q8n2f4	homo sapien
615	111.5	5.3	508	2	Q96LA5	Q96la5	homo sapien

No.	V1	V2	Len	T	ID	Accession	Organism
616	111.5	5.3	816	2	Q8NFA5	Q8nfa5	homo sapien
617	111.5	5.3	869	1	MUSK_HUMAN	O15146	homo sapien
618	111.5	5.3	1060	2	Q9QZI3	Q9qzi3	rattus norv
619	111.5	5.3	1070	2	Q61Q54	Q61q54	homo sapien
620	111	5.3	252	2	Q8WWT6	Q8wwt6	mus musculu
621	111	5.3	283	2	Q8K091	Q8k091	homo sapien
622	111	5.3	395	2	Q8BXJ7	Q8bxj7	m mus muscu
623	111	5.3	395	2	Q8BZP4	Q8bzp4	homo sapien
624	111	5.3	960	2	Q7PV74	Q7pv74	anopheles g
625	111	5.3	1026	2	Q81WV2	Q81wv2	homo sapien
626	111	5.3	1228	2	Q8MRA3	Q8mra3	drosophila
627	111	5.3	1235	2	Q86BD5	Q86bd5	drosophila
628	111	5.3	1235	2	Q9V787	Q9v787	drosophila
629	111	5.3	6632	1	UN89_CAEEL	O01761	caenorhabdi
630	111	5.3	8081	2	Q7Z120	Q7z120	homo sapien
631	110.5	5.3	316	2	Q8WP58	Q8wp58	drosophila
632	110.5	5.3	370	2	Q6MZQ3	Q6mzq3	homo sapien
633	110.5	5.3	390	2	Q96AP7	Q96ap7	homo sapien
634	110.5	5.3	390	2	Q96T50	Q96t50	homo sapien
635	110.5	5.3	395	2	Q61E78	Q61e78	paralichthy
636	110.5	5.3	404	2	Q8BYP1	Q8byp1	mus musculu
637	110.5	5.3	422	2	Q96PJ3	Q96pj3	homo sapien
638	110.5	5.3	500	2	Q6UX41	Q6ux41	homo sapien
639	110.5	5.3	513	2	O00481	O00481	homo sapien
640	110.5	5.3	515	2	Q96RE0	Q96re0	homo sapien
641	110.5	5.3	515	2	Q96PJ5	Q96pj5	homo sapien
642	110.5	5.3	544	2	Q6UX18	Q6ux18	homo sapien
643	110.5	5.3	546	2	Q80X70	Q80x70	mus musculu
644	110.5	5.3	548	2	Q99NB3	Q99nb3	mus musculu
645	110.5	5.3	662	2	Q8MQ29	Q8mq29	drosophila
646	110.5	5.3	662	2	Q9VGD0	Q9vgd0	drosophila
647	110.5	5.3	789	1	KIRI_RAT	Q9JHX9	rattus norv
648	110.5	5.3	800	2	Q7Q0X2	Q7q0x2	anopheles g
649	110.5	5.3	1889	2	Q96MC6	Q96mc6	homo sapien
650	110	5.2	218	2	Q96PJ6	Q96pj6	homo sapien
651	110	5.2	428	2	Q7SX76	Q7sx76	brachydanio
652	110	5.2	483	1	MAG_RAT	P07722	rattus norv
653	110	5.2	626	2	Q7RTW3	Q7rtw3	homo sapien
654	110	5.2	637	2	Q6RCF4	Q6rcf4	vibriophage
655	110	5.2	741	2	Q8AYP3	Q8ayp3	brachydanio
656	110	5.2	815	1	NCM2_HUMAN	Q15394	homo sapien
657	109.5	5.2	837	1	ROB2_HUMAN	Q9HCK4	homo sapien
658	109.5	5.2	1378	2	Q8NI14	Q8ni14	homo sapien
659	109.5	5.2	1391	2	O18465	O18465	hirudo medi
660	109.5	5.2	1880	2	Q6BEQ6	Q6beq6	caenorhabdi
661	109.5	5.2	2389	2	O54947	O54947	rattus norv
662	109.5	5.2	307	2	Q9BD88	Q9bd88	cercocebus
663	109.5	5.2	323	2	Q819N0	Q819n0	branchiosto
664	109.5	5.2	334	2	Q90720	Q90720	gallus gall
665	109.5	5.2	345	2	Q7TSI8	Q7tsi8	mus musculu
666	109.5	5.2	349	1	OPCM_RAT	P31997	rattus norv
667	109.5	5.2	383	1	CEA8_HUMAN	Q7QBC5	homo sapien
668	109.5	5.2	477	2	Q6UXJ4	Q6uxj4	homo sapien
669	109.5	5.2	526	1	BUTY_HUMAN	Q13410	homo sapien
670	109.5	5.2	526	2	Q9H458	Q9h458	homo sapien
671	109.5	5.2	548	2	Q92133	Q92133	rattus norv
672	109.5	5.2	595	2	Q90720	Q90720	gallus gall
673	109.5	5.2	800	2	Q7TEI8	Q7tei8	mus musculu
674	109.5	5.2	801	2	Q61851	Q61851	mus musculu
675	109.5	5.2	1336	1	FGR3_MOUSE	P53767	mus musculu
676	109.5	5.2	1465	1	VGR1_RAT	P53767	rattus norv
677	109	5.2	263	2	Q7TQG5	Q7tqg5	mus musculu
678	109	5.2	283	2	Q7TPW5	Q7tpw5	mus musculu
679	109	5.2	283	2	Q7TPH5	Q7tph5	mus musculu
680	109	5.2	292	2	Q7TSP5	Q7tsp5	mus musculu
681	109	5.2	328	2	Q7TEP5	Q7tep5	mus musculu
682	109	5.2	345	2	Q6UY47	Q6uy47	mus musculu
683	109	5.2	417	2	Q88775	Q88775	rattus norv
684	109	5.2	562	2	Q7PVU1	Q7pvu1	anopheles g
685	109	5.2	582	1	PVR_HUMAN	P15151	homo sapien
686	109	5.2	595	2	Q6YNR7	Q6ynr7	brachydanio
687	109	5.2	640	2	Q80WN2	Q80wn2	mus musculu
688	109	5.2	646	1	Q88SM2	MU18_HUMAN	homo sapien

No.					Accession	Accession	Species
689	109	5.2	646	2	Q6PHR3	Q6phr3	homo sapien
690	109	5.2	1106	2	Q8WX93	Q8wx93	homo sapien
691	108.5	5.2	345	1	P11834	P11834	bos taurus
692	108.5	5.2	348	1	OPCM_BOVIN	OPCM_BOVIN	bos taurus
693	108.5	5.2	348	1	NEGR_MOUSE	NEGR_MOUSE	mus musculu
694	108.5	5.2	416	2	Q7M048	Q7m048	rattus norv
695	108.5	5.2	495	2	Q9HCY1	Q9hcy1	homo sapien
696	108.5	5.2	686	1	SILB_HUMAN	SILB_HUMAN	homo sapien
697	108.5	5.2	705	2	Q8CBD3	Q8cbd3	mus musculu
698	108.5	5.2	757	1	Q96J84	Q96j84	homo sapien
699	108.5	5.2	807	2	KIR1_HUMAN	KIR1_HUMAN	homo sapien
700	108.5	5.2	818	2	Q6DD66	Q6dd66	xenopus lae
701	108.5	5.2	819	1	Q9PSV9	Q9psv9	xenopus lae
702	108.5	5.2	868	1	FGR1_CHICK	FGR1_CHICK	gallus gall
703	108.5	5.2	878	2	MUSK_MOUSE	MUSK_MOUSE	mus musculu
704	108.5	5.2	898	2	Q9GV22	Q9gv22	mytilus gal
705	108.5	5.2	1021	2	Q69Z26	Q69z26	mus musculu
706	108.5	5.2	1028	2	Q9U052	Q9u052	homo sapien
707	108.5	5.2	1114	2	Q9BWV1	Q9bwv1	homo sapien
708	108.5	5.2	1115	2	Q6UXJ5	Q6uxj5	homo sapien
709	108.5	5.2	1328	2	Q21043	Q21043	caenorhabdi
710	108.5	5.2	1426	2	Q82ZI1	Q82zi1	enterococcu
711	108.5	5.2	2000	2	O97791	O97791	oryctolagus
712	108.5	5.2	2169	2	Q8AV58	Q8av58	gallus gall
713	108.5	5.2	4203	2	Q96SG2	Q96sg2	caenorhabdi
714	108.5	5.2	4219	2	Q9NL87	Q9nl87	caenorhabdi
715	108.5	5.2	4369	2	Q8MXD7	Q8mxd7	caenorhabdi
716	108.5	5.2	4447	2	Q8MXD8	Q8mxd8	caenorhabdi
717	108.5	5.2	4488	2	O90271	O90271	branchiosto
718	108.5	5.2	4736	2	Q9TXK2	Q9txk2	brachydanio
719	108	5.1	173	2	Q7YT99	Q7yt99	mytilus gal
720	108	5.1	286	1	Q9JKD5	Q9jkd5	rattus norv
721	108	5.1	325	1	O46535	O46535	bos taurus
722	108	5.1	329	2	O95791	O95791	homo sapien
723	108	5.1	333	2	Q8HW98	Q8hw98	mus musculu
724	108	5.1	376	2	Q8N225	Q8n225	homo sapien
725	108	5.1	407	2	O8I9N2	O8i9n2	branchiosto
726	108	5.1	509	2	Q90Z71	Q90z71	brachydanio
727	108	5.1	526	1	Q9D2J4	Q9d2j4	mus musculu
728	108	5.1	605	2	Q9EQY5	Q9eqy5	caenorhabdi
729	108	5.1	614	2	BUTY_BOVIN	BUTY_BOVIN	bos taurus
730	108	5.1	868	1	Q6GNL9	Q6gnl9	xenopus lae
731	108	5.1	879	1	Q6DDQ7	Q6ddq7	xenopus lae
732	108	5.1	922	1	MUSK_RAT	MUSK_RAT	rattus norv
733	108	5.1	1098	1	FPRP_RAT	FPRP_RAT	rattus norv
734	108	5.1	1099	1	Q9O413	Q9o413	brachydanio
735	108	5.1	1109	2	PGDR_MOUSE	PGDR_MOUSE	mus musculu
736	108	5.1	1110	2	P97527	P97527	rattus norv
737	108	5.1	1150	2	Q8CE91	Q8ce91	mus musculu
738	108	5.1	1244	2	Q8CE73	Q8ce73	mus musculu
739	108	5.1	1612	1	Q8BS24	Q8bs24	mus musculu
740	108	5.1	2325	2	Q69YJ3	Q69yj3	homo sapien
741	107.5	5.1	278	2	ROB1_MOUSE	ROB1_MOUSE	mus musculu
742	107.5	5.1	350	2	Q9QYL3	Q9qyl3	caenorhabdi
743	107.5	5.1	366	2	Q99420	Q99420	mus musculu
744	107.5	5.1	402	1	Q819N1	Q819n1	branchiosto
745	107.5	5.1	429	2	Q8N759	Q8n759	homo sapien
746	107.5	5.1	531	2	HPI4_HUMAN	HPI4_HUMAN	homo sapien
747	107.5	5.1	659	2	Q96LA6	Q96la6	homo sapien
748	107.5	5.1	660	1	Q659F2	Q659f2	homo sapien
749	107.5	5.1	789	2	Q62NM1	Q62nm1	homo sapien
750	107.5	5.1	800	2	Q7Z681	Q7z681	homo sapien
751	107.5	5.1	818	1	KIR1_MOUSE	KIR1_MOUSE	mus musculu
752	107.5	5.1	828	2	Q99052	Q99052	mus musculu
753	107.5	5.1	846	2	Q91742	Q91742	mus musculu
754	107.5	5.1	1026	2	Q91743	Q91743	xenopus lae
755	107.5	5.1	1100	2	O57577	O57577	xenopus lae
756	107.5	5.1	1225	2	Q62845	Q62845	rattus norv
757	107.5	5.1	1235	2	O57576	O57576	cynops pyrr
758	107.5	5.1	199	2	Q6GP61	Q6gp61	cynops pyrr
759	107.5	5.1	332	2	O95428	O95428	xenopus lae
760	107	5.1	199	2	O8NDI0	O8ndi0	homo sapien
761	107	5.1	332	2	Q6UXG3	Q6uxg3	homo sapien
762	107	5.1	442	2	Q6KAT6	Q6kat6	mus musculu
763	107	5.1	515	1	PVR1_MOUSE	PVR1_MOUSE	mus musculu
764	107	5.1	515	2	Q99KF6	Q99kf6	mus musculu
765	107	5.1	606	2	Q6P9M9	Q6p9m9	mus musculu
766	107	5.1	622	2	Q9ES88	Q9es88	rattus norv
767	107	5.1	648	2	Q9ESS8	Q9ess8	rattus norv
768	107	5.1	817	2	Q9JKB2	Q9jkb2	mus musculu
769	107	5.1	879	1	FPRP_MOUSE	FPRP_MOUSE	mus musculu
770	107	5.1	2558	1	Q9NR91	Q9nr91	homo sapien
771	107	5.1	19066	2	Q801W8	Q801w8	mus musculu
772	106.5	5.1	304	2	Q9CVA4	Q9cva4	brachydanio
773	106.5	5.1	354	2	Q28381	Q28381	mus musculu
774	106.5	5.1	404	2	HPI1_HORSE	HPI1_HORSE	equus cabal
775	106.5	5.1	437	2	Q8BLQ9	Q8blq9	homo sapien
776	106.5	5.1	662	2	O86YV1	O86yv1	homo sapien
777	106.5	5.1	719	1	O60926	O60926	drosophila
778	106.5	5.1	793	2	Q904G1	Q904g1	mus musculu
779	106.5	5.1	813	1	Q8BQC3	Q8bqc3	mus musculu
780	106.5	5.1	822	2	P11362	P11362	homo sapien
781	106.5	5.1	1227	2	Q21038	Q21038	caenorhabdi
782	106.5	5.1	1232	2	Q90284	Q90284	mus musculu
783	106.5	5.1	1474	2	Q8T4M0	Q8t4m0	carassius a
784	106.5	5.1	1509	1	Q81PG1	Q81pg1	drosophila
785	106.5	5.1	1509	1	Q95P10	Q95p10	drosophila
786	106	5.1	317	2	Q8BEK4	Q8bek4	caenorhabdi
787	106	5.1	381	2	Q8R4B1	Q8r4b1	mus musculu
788	106	5.1	796	2	Q91287	Q91287	pleurodeles
789	106	5.1	919	1	O10656	O10656	caenorhabdi
790	106	5.1	1040	2	EG15_CAEEL	EG15_CAEEL	caenorhabdi
791	106	5.1	1051	2	Q7JL68	Q7jl68	caenorhabdi
792	106	5.1	1081	2	Q92CT7	Q92ct7	caenorhabdi
793	106	5.1	1096	2	Q8MQ14	Q8mq14	caenorhabdi
794	106	5.1	1099	2	O70EG7	O70eg7	mus musculu
795	106	5.1	1185	2	Q8AYZ8	Q8ayz8	anopheles g
796	106	5.1	1388	2	Q8BEI5	Q8bei5	variola vir
797	106	5.1	1409	2	Q92I09	Q92i09	variola vir
798	106	5.1	1409	1	Q6UXG0	Q6uxg0	mus musculu
799	106	5.1	1428	2	Q6TGK9	Q6tgk9	homo sapien
800	106	5.1	1914	1	Q8K094	Q8k094	oryctolagus
801	106	5.1	1914	2	Q91WP1	Q91wp1	m hypotheti
802	106	5.1	2222	2	Q8BVF6	Q8bvf6	mus musculu
803	105.5	5.0	318	2	Q62TR2	Q62tr2	mus musculu
804	105.5	5.0	318	2	Q96CJ3	Q96cj3	homo sapien
805	105.5	5.0	328	2	Q63827	Q63827	homo sapien
806	105.5	5.0	394	2	Q60818	Q60818	rattus norv
807	105.5	5.0	394	2	Q80T10	Q80t10	homo sapien
808	105.5	5.0	408	2	Q28260	Q28260	homo sapien
809	105.5	5.0	408	2	Q7PME2	Q7pme2	mus musculu
810	105.5	5.0	408	2	Q8CIM9	Q8cim9	mus musculu
811	105.5	5.0	408	2	P16092	P16092	mus musculu
812	105.5	5.0	527	2	Q04589	Q04589	mus musculu
813	105.5	5.0	601	2	Q60818	Q60818	homo sapien
814	105.5	5.0	729	2	Q8CFK8	Q8cfk8	homo sapien
815	105.5	5.0	731	2	Q60830	Q60830	rattus norv
816	105.5	5.0	733	2	Q80T10	Q80t10	mus musculu
817	105.5	5.0	733	2	Q28260	Q28260	mus musculu
818	105.5	5.0	739	2	Q7PME2	Q7pme2	mus musculu
819	105.5	5.0	789	2	Q8CIM9	Q8cim9	homo sapien
820	105.5	5.0	822	2	Q91WP6	Q91wp6	anopheles g
821	105.5	5.0	822	2	Q8BVF6	Q8bvf6	mus musculu
822	105.5	5.0	822	1	Q62TR2	Q62tr2	rattus norv
823	105.5	5.0	987	2	Q96CJ3	Q96cj3	homo sapien
824	105.5	5.0	1036	2	Q60818	Q60818	homo sapien
825	105.5	5.0	1102	2	Q8CFK8	Q8cfk8	mus musculu
826	105.5	5.0	1215	2	Q7YZM8	Q7yzm8	homo sapien
827	105.5	5.0	1215	2	Q8SWW3	Q8sww3	drosophila
828	105.5	5.0	1256	2	Q923W7	Q923w7	drosophila
829	105.5	5.0	1390	2	Q7KTI7	Q7kti7	rattus norv
830	105.5	5.0	1461	2	Q8T9F6	Q8t9f6	drosophila
831	105	5.0	1503	2	O35158	O35158	drosophila
832	105	5.0	1509	2	Q8BZ274	Q8bz274	macaca mula
833	105	5.0	232	2	Q8MZE4	Q8mze4	mus musculu
834	105	5.0	145	2	Q9VT83	Q9vt83	drosophila

#	V1	V2	N1	N2	Accession	Species
835	105	5.0	509	2	Q91YK7	mus musculu
836	105	5.0	622	2	Q9ESS5	mus musculu
837	105	5.0	622	2	Q9R069	mus musculu
838	105	5.0	626	1	MAG_MOUSE	mus musculu
839	105	5.0	645	2	Q7RTW4	homo sapien
840	105	5.0	646	2	Q95812	homo sapien
841	105	5.0	650	2	Q99K86	mus musculu
842	105	5.0	708	1	KIR2_HUMAN	homo sapien
843	105	5.0	739	2	Q86FP2	oryctolagus
844	105	5.0	810	2	Q9PS96	xenopus lae
845	105	5.0	862	1	P35329	mus musculu
846	105	5.0	940	2	Q8NFA7	homo sapien
847	105	5.0	998	2	Q977Y2	thermoplasm
848	105	5.0	4816	2	Q8TL03	bombyx mori
849	104.5	5.0	265	2	O02280	caenorhabdi
850	104.5	5.0	360	2	Q8MRE6	drosophila
851	104.5	5.0	377	2	Q8OVO4	mus musculu
852	104.5	5.0	426	2	Q64HX5	oncorhynchu
853	104.5	5.0	428	2	Q6F3J3	mus musculu
854	104.5	5.0	454	2	Q6DD85	homo sapien
855	104.5	5.0	523	2	Q8K2H7	mus musculu
856	104.5	5.0	536	2	Q8BJE2	mus musculu
857	104.5	5.0	538	2	Q9QYQ7	mus musculu
858	104.5	5.0	582	2	Q95N25	homo sapien
859	104.5	5.0	640	2	Q8BGH8	m mus muscu
860	104.5	5.0	640	2	O8C031	mus musculu
861	104.5	5.0	722	2	Q6GNB3	xenopus lae
862	104.5	5.0	920	2	Q9P232	homo sapien
863	104.5	5.0	931	2	Q6KAM5	homo sapien
864	104.5	5.0	1026	2	Q94780	homo sapien
865	104.5	5.0	1100	2	Q94779	homo sapien
866	104.5	5.0	1109	2	Q6AZB0	mus musculu
867	104.5	5.0	1184	2	O75339	homo sapien
868	104.5	5.0	1184	2	Q6UW99	homo sapien
869	104.5	5.0	1377	1	ALC_RABIT	oryctolagus
870	104.5	5.0	1461	1	NEO1_RAT	rattus norv
871	104.5	5.0	1503	2	Q92859	homo sapien
872	104.5	5.0	2222	2	Q97394	drosophila
873	104.5	5.0	2230	2	Q86BQ7	drosophila
874	104.5	5.0	2693	2	Q8ISF3	caenorhabdi
875	104.5	5.0	2708	2	Q8ISF4	caenorhabdi
876	104.5	5.0	18519	2	Q8ISF6	caenorhabdi
877	104.5	5.0	18534	2	Q8ISF7	caenorhabdi
878	104	5.0	299	1	P01879	oryctolagus
879	104	5.0	334	1	Q9NR44	homo sapien
880	104	5.0	524	1	BUTY_MOUSE	mus musculu
881	104	5.0	524	1	Q921K7	mus musculu
882	104	5.0	600	2	Q8N7W7	homo sapien
883	104	5.0	662	1	NRG1_RAT	rattus norv
884	104	5.0	694	2	Q8SWT7	drosophila
885	104	5.0	734	2	Q96LA4	homo sapien
886	104	5.0	740	2	Q96P29	homo sapien
887	104	5.0	812	2	Q69ZJ6	mus musculu
888	104	5.0	994	1	MERK_RAT	rattus norv
889	104	5.0	998	2	Q9W4Y6	drosophila
890	104	5.0	1356	1	VGR2_HUMAN	homo sapien
891	104	4.9	147	2	Q8CFJ3	mus musculu
892	103.5	4.9	275	2	Q9BDN9	homo sapien
893	103.5	4.9	280	2	Q8UWK1	ictalurus p
894	103.5	4.9	287	2	Q9QW80	mus sp.
895	103.5	4.9	356	1	HPL1_MOUSE	mus musculu
896	103.5	4.9	376	2	Q9QW78	mus sp. f
897	103.5	4.9	413	2	Q69PO	antheraea f
898	103.5	4.9	592	2	Q9LN5	mus musculu
899	103.5	4.9	628	2	P50895	homo sapien
900	103.5	4.9	628	1	Q86VC7	homo sapien
901	103.5	4.9	677	1	NRG1_XENLA	xenopus lae
902	103.5	4.9	799	2	Q8C3V5	homo sapien
903	103.5	4.9	799	2	Q8CIB8	mus musculu
904	103.5	4.9	824	2	Q91286	mus musculu
905	103.5	4.9	847	1	CD22_HUMAN	homo sapien
906	103.5	4.9	998	2	Q9SR27	drosophila
907	103.5	4.9	1030	2	Q8NFA8	homo sapien
908	103.5	4.9	1145	2	Q9BKL8	aplysia cal
909	103.5	4.9	1331	2	Q7Q623	anopheles g
910	103.5	4.9	1513	2	Q90270	brachydanio
911	103.5	4.9	1651	2	Q9Y6N7	homo sapien
912	103.5	4.9	6048	2	Q7JN85	caenorhabdi
913	103.5	4.9	6839	2	Q23550	caenorhabdi
914	103.5	4.9	7158	2	Q23551	caenorhabdi
915	103	4.9	229	2	Q7PUC4	anopheles g
916	103	4.9	415	2	Q60977	mus musculu
917	103	4.9	498	2	Q8BBT6	mus musculu
918	103	4.9	606	2	Q61RH8	rattus norv
919	103	4.9	763	2	Q95YM9	halocynthia
920	103	4.9	771	1	PIGR_MOUSE	mus musculu
921	103	4.9	873	1	FAS2_DROME	drosophila
922	103	4.9	1470	1	ROB2_MOUSE	mus musculu
923	103	4.9	1742	2	Q24463	drosophila
924	102.5	4.9	224	2	Q66GV2	xenopus lae
925	102.5	4.9	308	2	Q6PNM1	rattus norv
926	102.5	4.9	318	2	Q8BEI6	variola vir
927	102.5	4.9	318	2	Q9QNG4	macaca mula
928	102.5	4.9	323	2	Q9BDM4	macaca mula
929	102.5	4.9	354	1	HPL1_RAT	rattus norv
930	102.5	4.9	356	2	Q819K2	branchiosto
931	102.5	4.9	399	2	Q7QCH7	anopheles g
932	102.5	4.9	413	2	Q27418	manduca sex
933	102.5	4.9	423	2	Q9WRU4	macaca mula
934	102.5	4.9	636	2	Q7LON3	homo sapien
935	102.5	4.9	640	2	Q9HCJ2	homo sapien
936	102.5	4.9	992	2	Q9CQL5	homo sapien
937	102.5	4.9	1176	1	KMLS_BOVIN	bos taurus
938	102.5	4.9	1184	2	Q28824	homo sapien
939	102.5	4.9	1651	1	ROB1_RAT	rattus norv
940	102	4.9	305	2	Q62S95	homo sapien
941	102	4.9	314	2	Q8BEK8	vaccinia vi
942	102	4.9	319	1	O00477	homo sapien
943	102	4.9	332	2	Q8TA95	homo sapien
944	102	4.9	332	2	Q9BU81	homo sapien
945	102	4.9	334	2	Q76PA0	homo sapien
946	102	4.9	350	2	Q8MS24	drosophila
947	102	4.9	357	2	O15338	homo sapien
948	102	4.9	359	2	P78410	homo sapien
949	102	4.9	461	2	O35947	mesocricetu
950	102	4.9	504	2	Q6NNA1	homo sapien
951	102	4.9	508	2	Q9VGD2	drosophila
952	102	4.9	523	2	O00480	homo sapien
953	102	4.9	626	2	Q9VGD3	drosophila
954	102	4.9	664	1	MAG_HUMAN	homo sapien
955	102	4.9	702	1	CEA5_HUMAN	homo sapien
956	102	4.9	702	2	Q8N4D0	homo sapien
957	102	4.9	733	2	Q8SQ83	drosophila
958	102	4.9	883	2	Q8TTT9	methanosarc
959	102	4.9	1032	2	Q8AXZ4	brachydanio
960	102	4.9	1098	2	Q961D6	drosophila
961	102	4.9	1249	2	Q77MZ9	rattus norv
962	102	4.9	1271	2	Q9BNI7	gallus gall
963	102	4.9	1332	2	MYPC_CHICK	gallus gall
964	102	4.9	1332	2	Q9VOW7	drosophila
965	101.5	4.8	323	2	Q9BDM9	homo sapien
966	101.5	4.8	413	2	Q9BDN9	macaca neme
967	101.5	4.8	423	2	Q26438	hyalophora
968	101.5	4.8	520	2	Q9J2M8	rhesus monk
969	101.5	4.8	606	2	Q7Z3M6	homo sapien
970	101.5	4.8	624	2	Q9VNM6	drosophila
971	101.5	4.8	639	2	Q9ESS6	rattus norv
972	101.5	4.8	742	2	Q6P830	homo sapien
973	101.5	4.8	802	2	Q8N6S2	homo sapien
974	101.5	4.8	898	2	Q8TDA0	homo sapien
975	101.5	4.8	912	2	Q8CDA0	homo sapien
976	101.5	4.8	1005	1	FAS2_SCHAM	schistocerc
977	101.5	4.8	1184	2	P22648	oryctolagus
978	101.5	4.8	1194	1	ICA5_RABIT	oryctolagus
979	101.5	4.8	1214	1	P79921	xenopus lae
980	101.5	4.8	1214	2	Q66K08	mus musculu
981	101.5	4.8	1214	2	Q7TPV3	mus musculu
982	101.5	4.8	1250	2	Q8BV01	mus musculu

Rank	Score	E	Length	N	ID	Accession	Organism
981	101.5	4.8	1260	1	CAML_MOUSE	P11627	mus musculu
982	101.5	4.8	1450	2	Q7CP2	Q7qcp2	anopheles g
983	101.5	4.8	1526	2	Q94538	Q94538	drosophila
984	101	4.8	298	2	Q9GL74	Q9gl74	cercopithec
985	101	4.8	300	2	Q8BEK0	Q8bek0	cowpox viru
986	101	4.8	327	2	Q6PCB8	Q6pcb8	homo sapien
987	101	4.8	478	2	Q6IQ4	Q6iq4	xenopus lae
988	101	4.8	507	2	Q6K90	Q6k90	homo sapien
989	101	4.8	584	2	Q90989	Q90989	gallus gall
990	101	4.8	605	2	Q8TBU0	Q8tbu0	homo sapien
991	101	4.8	620	1	SMP_COTJA	Q22154	coturnix co
992	101	4.8	626	2	Q90880	Q90880	gallus gall
993	101	4.8	648	2	Q9EPF1	Q9epf1	mus musculu
994	101	4.8	673	2	Q6MZW2	Q6mzw2	homo sapien
995	101	4.8	693	2	Q9UPU1	Q9upu1	homo sapien
996	101	4.8	700	1	KIR2_MOUSE	Q6tsu7	mus musculu
997	101	4.8	701	2	Q90330	Q90330	coturnix co
998	101	4.8	713	2	Q6P1M7	Q6p1m7	homo sapien
999	101	4.8	743	1	TYO3_HUMAN	P91644	homo sapien
1000	101	4.8	890	2	Q86VR3	Q86vr3	homo sapien
1001	101	4.8	890	1	P91644	P91644	drosophila
1002	101	4.8	892	2	Q06418	Q06418	homo sapien
1003	101	4.8	1040	2	Q9W675	Q9w675	brachydanio
1004	101	4.8	1214	2	O75054	O75054	homo sapien
1005	101	4.8	1377	2	Q94537	Q94537	drosophila
1006	101	4.8	1944	2	Q69SL3	Q69sl3	brachydanio
1007	101	4.8	3287	2	Q7S9K4	Q7s9k4	neurospora
1008	100.5	4.8	6620	2	Q96AA2	Q96aa2	homo sapien
1009	100.5	4.8	280	2	Q8UWL1	Q8uwl1	ictalurus p
1010	100.5	4.8	288	2	Q22385	Q22385	caenorhabdi
1011	100.5	4.8	333	2	Q90241	Q90241	gallus gall
1012	100.5	4.8	337	2	Q6GL27	Q6gl27	xenopus lae
1013	100.5	4.8	355	1	HPL1_CHICK	P07354	gallus gall
1014	100.5	4.8	370	2	Q80OY8	Q80oy8	brachydanio
1015	100.5	4.8	413	1	HEMO_HYACE	P25033	hyalophora
1016	100.5	4.8	455	2	Q9UIR0	Q9uir0	homo sapien
1017	100.5	4.8	500	2	Q9XZB7	Q9xzb7	drosophila
1018	100.5	4.8	525	2	Q7QJK5	Q7qjk5	anopheles g
1019	100.5	4.8	606	2	Q9ESS7	Q9ess7	mus musculu
1020	100.5	4.8	700	1	MEPB_HUMAN	Q16820	homo sapien
1021	100.5	4.8	802	1	FGR4_HUMAN	P22455	homo sapien
1022	100.5	4.8	814	2	Q8EC41	Q8ec41	shewanella
1023	100.5	4.8	876	2	Q7PW78	Q7pw78	anopheles g
1024	100.5	4.8	906	2	Q8TPY9	Q8tpy9	methanosarc
1025	100.5	4.8	1250	2	Q88971	Q88971	mus musculu
1026	100.5	4.8	1252	2	Q9EQS9	Q9eqs9	mus musculu
1027	100.5	4.8	1253	2	Q9EQS8	Q9eqs8	mus musculu
1028	100.5	4.8	307	2	Q94431	Q94431	ciona intes
1029	100.5	4.8	314	2	Q8BEK7	Q8bek7	vaccinia vi
1030	100	4.8	322	1	ICOL_MOUSE	P42081	mus musculu
1031	100	4.8	329	1	CD86_HUMAN	Q9TTF2	homo sapien
1032	100	4.8	329	2	Q9TTF2	Q9ttf2	canis famil
1033	100	4.8	354	1	HPL1_HUMAN	P10915	homo sapien
1034	100	4.8	400	2	Q8C5E4	Q8c5e4	mus musculu
1035	100	4.8	458	1	CD4_PANTR	P16004	pan troglod
1036	100	4.8	493	2	Q6PSY4	Q6psy4	homo sapien
1037	100	4.8	504	2	Q98923	Q98923	gallus gall
1038	100	4.8	584	2	O00478	O00478	homo sapien
1039	100	4.8	584	2	Q98921	Q98921	gallus gall
1040	100	4.8	626	2	Q98922	Q98922	gallus gall
1041	100	4.8	669	2	Q6B515	Q6b515	poephila gu
1042	100	4.8	684	2	Q7SEG1	Q7seg1	neurospora
1043	100	4.8	734	2	Q96P31	Q96p31	homo sapien
1044	100	4.8	784	2	Q81063	Q81063	drosophila
1045	100	4.8	818	1	TRKB_CHICK	Q91987	gallus gall
1046	100	4.8	842	1	UN5A_HUMAN	Q6zn44	homo sapien
1047	100	4.8	894	2	Q9VKG1	Q9vkg1	drosophila
1048	100	4.8	1014	1	Q8NFA6	Q8nfa6	homo sapien
1049	99.5	4.8	295	2	Q9GL75	Q9gl75	drosophila
1050	99.5	4.8	416	2	Q96360	Q96360	hyphantria
1051	99.5	4.7	432	2	Q6DDE7	Q6dde7	xenopus lae
1052	99.5	4.7	459	1	CD4_RABIT	P46630	oryctolagus
1053	99.5	4.7	476	2	Q80WU0	Q80wu0	mus musculu
1054	99.5	4.7	500	2	Q9W260	Q9w260	drosophila
1055	99.5	4.7	549	2	Q6PFC5	Q6pfc5	mus musculu
1056	99.5	4.7	738	1	TRKB_MOUSE	P79390	bos primige
1057	99.5	4.7	821	2	P15209	P15209	mus musculu
1058	99.5	4.7	939	2	Q9VB85	Q9vb85	drosophila
1059	99.5	4.7	1009	2	Q93250	Q93250	xenopus lae
1060	99.5	4.7	1019	2	Q8BJK6	Q8bjk6	mus musculu
1061	99.5	4.7	1021	2	Q93033	Q93033	homo sapien
1062	99.5	4.7	1028	2	Q62682	Q62682	rattus norv
1063	99.5	4.7	1031	2	Q80XN7	Q80xn7	mus musculu
1064	99.5	4.7	1252	2	Q9JLI1	Q9jli1	mus musculu
1065	99.5	4.7	1256	2	Q9JIX1	Q9jix1	mus musculu
1066	99.5	4.7	1379	2	P79701	P79701	coturnix co
1067	99.5	4.7	1569	2	Q6PAC0	Q6pac0	homo sapien
1068	99.5	4.7	1666	2	MYM1_MOUSE	Q62191	mus musculu
1069	99.5	4.7	2021	2	Q62191	Q62191	mus musculu
1070	99.5	4.7	6084	2	Q81ZQ9	Q81zq9	homo sapien
1071	99	4.7	234	2	Q87ID8	Q87id8	vibrio para
1072	99	4.7	275	1	CD4_HUMAN	P01730	homo sapien
1073	99	4.7	275	2	V05S_FOWPV	Q70H96	fowlpox vir
1074	99	4.7	313	2	Q70H96	Q70h96	fowlpox vir
1075	99	4.7	313	2	P21975	P21975	fowlpox vir
1076	99	4.7	359	1	HPL3_MOUSE	O35531	variola vir
1077	99	4.7	458	2	O35531	O35531	rattus norv
1078	99	4.7	542	2	Q8NHN5	Q8nhn5	homo sapien
1079	99	4.7	621	2	Q8NFN5	Q8nfn5	homo sapien
1080	99	4.7	648	2	Q811T7	Q811t7	mus musculu
1081	99	4.7	756	2	Q8R2Y2	Q8r2y2	mus musculu
1082	99	4.7	773	2	Q80020	Q80020	brachydanio
1083	99	4.7	812	2	Q9NSW7	Q9nsw7	homo sapien
1084	99	4.7	831	2	FGR1_XENLA	P22182	xenopus lae
1085	99	4.7	891	2	Q71SY9	Q71sy9	gallus gall
1086	99	4.7	925	2	Q8BRX1	Q8brx1	mus musculu
1087	99	4.7	931	2	Q6CRA6	Q6cra6	kluyveromyc
1088	99	4.7	997	2	Q8NF26	Q8nf26	anopheles g
1089	99	4.7	1345	2	Q7PXX0	Q7pxx0	anopheles g
1090	99	4.7	1367	1	Q8VCD0	Q8vcd0	mus musculu
1091	99	4.7	1485	2	VGR2_MOUSE	P35918	mus musculu
1092	98.5	4.7	3197	2	Q6A031	Q6a031	mus musculu
1093	98.5	4.7	279	2	Q9WLD5	Q9wld5	drosophila
1094	98.5	4.7	283	2	Q9UD50	Q9ud50	homo sapien
1095	98.5	4.7	285	2	Q7QGT4	Q7qgt4	anopheles g
1096	98.5	4.7	309	2	Q7ZY30	Q7zy30	xenopus lae
1097	98.5	4.7	316	2	Q9YN57	Q9yn57	vaccinia vi
1098	98.5	4.7	413	1	Q7Q0P9	Q7q0p9	anopheles g
1099	98.5	4.7	482	2	HEMO_MANSE	P31398	manduca sex
1100	98.5	4.7	611	2	Q741A5	Q741a5	mycobacteri
1101	98.5	4.7	1333	1	Q8CVC7	Q8cvc7	streptococc
1102	98.5	4.7	1817	2	VGR1_MOUSE	P35969	mus musculu
1103	98	4.7	299	2	Q8I159	Q8i159	methanosarc
1104	98	4.7	302	1	Q70Q63	Q70q63	anopheles g
1105	98	4.7	347	2	ICOL_HUMAN	O75144	homo sapien
1106	98	4.7	381	2	Q9H730	Q9h730	homo sapien
1107	98	4.7	394	2	Q9Y4A4	Q9y4a4	homo sapien
1108	98	4.7	413	2	Q8HXR7	Q8hxr7	macaca fasc
1109	98	4.7	417	2	Q8HXR9	Q8hxr9	macaca mula
1110	98	4.7	492	2	Q8BGB4	Q8bgb4	m mus muscu
1111	98	4.7	569	2	Q7TNL1	Q7tnl1	mus musculu
1112	98	4.7	589	2	Q7QD44	Q7qd44	anopheles g
1113	98	4.7	628	2	Q8AXU1	Q8axu1	oncorhynchu
1114	98	4.7	645	2	Q8R366	Q8r366	mus musculu
1115	98	4.7	697	1	Q5R098	Q5r098	bos taurus
1116	98	4.7	824	1	SILA_HUMAN	Q9UDY8	homo sapien
1117	98	4.7	847	2	MLT1_HUMAN	Q8N475	homo sapien
1118	98	4.7	850	2	Q8N475	Q8n475	gallus gall
1119	98	4.7	880	1	Q9ULF7	Q9ulf7	homo sapien
1120	98	4.7	880	1	TYO3_MOUSE	P55146	mus musculu
1121	98	4.7	880	2	TYO3_RAT	P55144	rattus norv
1122	98	4.7	891	2	Q6NZM6	Q6nzm6	mus musculu
1123	98	4.7	931	2	Q9QY74	Q9qy74	mus musculu
1124	98	4.7	945	1	Q7C2S5	Q7c2s5	gallus gall
1125	98	4.7	945	2	UN5C_CHICK	O77589	gallus gall
1126	98	4.7	1499	2	Q90815	Q90815	equus cabal

Left table (ranks 1127–1199):

Rank	%	E	Len	N	Accession	Accession / Organism
1127	98	4.7	1878	2	Q6CP24	q6cp24 kluyveromyc
1128	98	4.7	1896	2	Q91AJ1	q91aj1 xenopus lae
1129	97.5	4.6	210	2	Q7PVL9	q7pvl9 anopheles g
1130	97.5	4.6	257	2	Q6NW92	q6nw92 brachydanio
1131	97.5	4.6	261	2	Q9W6V1	q9w6v1 gallus gall
1132	97.5	4.6	262	2	Q80170	q80170 mus musculu
1133	97.5	4.6	276	2	Q640S5	q640s5 xenopus tro
1134	97.5	4.6	313	2	Q90291	q90291 brachydanio
1135	97.5	4.6	316	2	Q8BEK1	q8bek1 cowpox viru
1136	97.5	4.6	354	1	Q8BEK1	p55252 bos taurus
1137	97.5	4.6	354	2	HPL1_PIG	p10859 sus scrofa
1138	97.5	4.6	354	1	HPL1_BOVIN	q29037 hydrochoeru
1139	97.5	4.6	418	2	Q29037	q9epn5 saimiri sci
1140	97.5	4.6	457	2	Q8HZT7	q8hzt7 saimiri sci
1141	97.5	4.6	457	1	CD4_SAISC	o06840 prevotella
1142	97.5	4.6	462	2	O06840	q83hs2 tropheryma
1143	97.5	4.6	473	2	Q83HS2	q83mx5 tropheryma
1144	97.5	4.6	473	2	Q83MX5	q6ehi2 rattus norv
1145	97.5	4.6	510	2	Q6EHI2	q86se4 homo sapien
1146	97.5	4.6	534	2	Q86SE4	q86t2 pan troglod
1147	97.5	4.6	534	2	Q86T2	q8wxj5 mus musculu
1148	97.5	4.6	553	2	Q8WXJ5	q95185 homo sapien
1149	97.5	4.6	571	2	Q8SPI8	q8spi8 sus scrofa
1150	97.5	4.6	571	1	ICCR_DROME	q00180 drosophila
1151	97.5	4.6	764	1	Q8MGQ1	q8mgq1 drosophila
1152	97.5	4.6	764	2	Q9W4U1	q9w4u1 drosophila
1153	97.5	4.6	764	1	Q81ZU9	q81zu9 homo sapien
1154	97.5	4.6	778	1	KIR3_HUMAN	q16620 mus musculu
1155	97.5	4.6	778	2	KIR3_MOUSE	homo sapien
1156	97.5	4.6	822	1	TRKB_HUMAN	q8wxj7 homo sapien
1157	97.5	4.6	838	2	Q8WXJ7	q78e87 mus musculu
1158	97.5	4.6	876	2	Q78E87	q95185 homo sapien
1159	97.5	4.6	876	1	UNSC_HUMAN	q674v1 podocoryne
1160	97.5	4.6	931	1	Q8Y337	q8y337 listeria mo
1161	97.5	4.6	931	1	Q7Q840	q7q840 anopheles g
1162	97.5	4.6	1254	2	NEO1_CHICK	q9610 gallus gall
1163	97.5	4.6	1348	2	Q9V6D5	q9v6d5 drosophila
1164	97	4.6	1383	1	MACP_MOUSE	q8wuk3 homo sapien
1165	97	4.6	1443	2	Q8WUK3	q7tst0 mus musculu
1166	97	4.6	1526	2	Q7TST0	q8uwl2 ictalurus p
1167	97	4.6	5327	1	Q8UWL2	q8bh36 mesocricetu
1168	97	4.6	240	2	Q8BH36	q9b26 macaca fasc
1169	97	4.6	249	2	Q9B26	q7pr66 anopheles g
1170	97	4.6	280	2	Q7PR66	q66607 equid herpe
1171	97	4.6	294	2	Q66607	p04217 equid herpe
1172	97	4.6	304	2	P04217	q8bja5 homo sapien
1173	97	4.6	305	2	Q8BJA5	q8nf28 homo sapien
1174	97	4.6	307	2	Q8HXR8	q8hxr8 cercopithec
1175	97	4.6	310	2	Q7PUM9	q7pum9 anopheles g
1176	97	4.6	317	2	Q6AF32	q6af32 leifsonia x
1177	97	4.6	388	1	A1BG_HUMAN	p04217 homo sapien
1178	97	4.6	393	2	Q8NF28	q8bja5 mus musculu
1179	97	4.6	456	2	Q8TC35	q8c35 homo sapien
1180	97	4.6	472	2	Q65XY2	q65xy2 caenorhabdi
1181	97	4.6	495	1	Q8MXU5	q8mxu5 caenorhabdi
1182	97	4.6	508	2	Q8WV47	p19320 homo sapien
1183	97	4.6	697	1	O39294	o39294 equid herpe
1184	97	4.6	703	2	Q8WV47	q8wv47 homo sapien
1185	97	4.6	724	2	Q8BFT0	q8bft0 m mus muscu
1186	97	4.6	739	1	PECI_PIG	q95242 sus scrofa
1187	97	4.6	740	1	O39294	q90749 gallus gall
1188	97	4.6	751	2	VCAL_HUMAN	q9uhw6 homo sapien
1189	97	4.6	804	2	Q9UHW6	p60756 rattus norv
1190	97	4.6	821	2	MDC1_RAT	q60805 mus musculu
1191	97	4.6	824	2	MERK_MOUSE	q07409 mus musculu
1192	97	4.6	891	1	KMLS_RABIT	p22294 oryctolagus
1193	97	4.6	949	2	Q95YK1	q95ykl ciona savig
1194	97	4.6	994	1	Q5YK1	q5yk1 homo sapien
1195	97	4.6	1028	2	Q6R2F7	q6r2f7 homo sapien
1196	97	4.6	1147	1	MYPC_HUMAN	o14896 homo sapien
1197	97	4.6	1177	2	Q9UM53	q9um53 homo sapien
1198	97	4.6	1274	1	O75129	o75129 homo sapien
1199	97	4.6	1274	2	Q8ML47	q8ml47 drosophila

Right table (ranks 1200–1272):

Rank	%	E	Len	N	Accession	Accession / Organism
1200	97	4.6	1860	2	Q7PQF4	q7pqf4 anopheles g
1201	96.5	4.6	187	2	Q8K4E4	q8k4e4 mus musculu
1202	96.5	4.6	193	2	Q7QGT6	q7qgt6 anopheles g
1203	96.5	4.6	313	1	Q85400	q85400 variola maj
1204	96.5	4.6	313	2	Q8AYZ7	q8ayz7 variola vir
1205	96.5	4.6	352	2	Q9W6V2	q9w6v2 gallus gall
1206	96.5	4.6	385	2	Q9UQF5	q9uqf5 homo sapien
1207	96.5	4.6	404	2	Q8TBZ1	q8tbz1 homo sapien
1208	96.5	4.6	510	2	Q8NDNS	q8ndns homo sapien
1209	96.5	4.6	625	2	O76536	o76536 strongyloce
1210	96.5	4.6	772	2	O86202	o86202 bacteriopha
1211	96.5	4.6	800	1	Q8TCG8	o8tcg8 homo sapien
1212	96.5	4.6	801	2	O70468	o70468 mus musculu
1213	96.5	4.6	804	2	Q9VBE5	q9vbe5 drosophila
1214	96.5	4.6	806	2	Q8FU04	q8fu04 corynebacte
1215	96.5	4.6	836	2	O80271	o80271 mus musculu
1216	96.5	4.6	893	2	Q8Y9T8	q8y9t8 listeria mo
1217	96.5	4.6	1200	1	Q9U8G8	q9u8g8 manduca sex
1218	96.5	4.6	1210	1	Q7PVK5	q7pvk5 anopheles g
1219	96.5	4.6	1232	2	Q9MCS7	q9mcs7 homo sapien
1220	96.5	4.6	1270	1	Q6P5S3	q6p5s3 homo sapien
1221	96.5	4.6	1304	2	Q8ML12	q8ml12 drosophila
1222	96.5	4.6	1421	2	Q7QK35	q7qk35 anopheles g
1223	96.5	4.6	1560	1	Q8BEI7	q8bei7 vaccinia vi
1224	96.5	4.6	2013	1	Q8BEJ2	q8bej2 rabbitpox v
1225	96.5	4.6	3198	2	Q8N732	q8n732 homo sapien
1226	96.5	4.6	3198	2	CD33_HUMAN	glc2_vibch
1227	96	4.6	228	2	GLC2_VIBCH	q6gm29 xenopus lae
1228	96	4.6	234	2	Q6GM29	q8rr31 vibrio fluv
1229	96	4.6	236	2	Q8RR31	q7pxi0 anopheles g
1230	96	4.6	252	2	Q7PXI0	q8caw4 mus musculu
1231	96	4.6	310	2	Q8CAW4	vcal_mouse
1232	96	4.6	310	2	P29533	q91x98 homo sapien
1233	96	4.6	312	2	Q91X98	q8ni16 anopheles g
1234	96	4.6	360	2	Q8NI16	q7qbl9 anopheles g
1235	96	4.6	364	2	Q7QBL9	q95m13 bos taurus
1236	96	4.6	407	2	Q95M13	q7jfl6 oryctolagus
1237	96	4.6	441	2	Q7JFL6	q9neg1 drosophila
1238	96	4.6	570	2	Q9NEG1	q6pa07 xenopus lae
1239	96	4.6	610	2	Q6PA07	q9vqw1 drosophila
1240	96	4.6	619	2	Q9VQW1	q80tb0 mus musculu
1241	96	4.6	732	2	Q80TB0	q977y4 enterococcu
1242	96	4.6	739	2	Q977Y4	q82yw8 clostridium
1243	96	4.6	739	2	Q82YW8	pgg2_rat
1244	96	4.6	771	2	PGG2_RAT	o00657 rattus norv
1245	96	4.6	773	2	O00657	q28733 homo sapien
1246	96	4.6	802	2	Q28733	p09326 homo sapien
1247	96	4.6	1016	2	P09326	cd48_human
1248	96	4.6	1035	2	CD48_HUMAN	q61a22 homo sapien
1249	96	4.6	1043	2	Q61A22	q6vzi1 aracatuba v
1250	96	4.6	1193	2	Q6VZI1	q8r2x9 cantagalo o
1251	96	4.6	1294	2	Q6QVZ1	q91zr9 homo sapien
1252	96	4.6	1483	2	Q91ZR9	q8r464 homo sapien
1253	95.5	4.6	1744	2	Q8R464	q9npp6 homo sapien
1254	95.5	4.6	2326	1	Q9NPP6	o01638 homo sapien
1255	95.5	4.6	6875	1	O01638	irl1_human
1256	95.5	4.6	220	1	IRL1_HUMAN	q6gn50 xenopus lae
1257	95.5	4.6	243	2	Q6GN50	q9uql3 homo sapien
1258	95.5	4.6	243	2	Q9UQL3	q86x29 homo sapien
1259	95.5	4.6	308	2	Q86X29	o70w32 oncorhynch
1260	95.5	4.6	308	2	O70W32	q70032 homo sapien
1261	95.5	4.6	388	2	Q86X29	q86x29 homo sapien
1262	95.5	4.6	416	2	Q8F6A9	q8f6a9 homo sapien
1263	95.5	4.6	556	1	Q8MJ27	q8mj27 leptospira
1264	95.5	4.6	573	2	LIB5_PANTR	lib5_pantr pan troglod
1265	95.5	4.6	591	2	Q8F6A9	q8f6a9 homo sapien
1266	95.5	4.6	601	2	Q8F6A9	q8f6a9 homo sapien
1267	95.5	4.6	611	1	Q922E0	q922e0 brachydanio
1268	95.5	4.6	643	2	Q800Y9	q800y9 brachydanio
1269	95.5	4.6	648	2	Q922E0	q922e0 mus musculu
1270	95.5	4.6	692	2	Q08481	q08481 mus musculu
1271	95.5	4.6	697	2	Q7QCU0	q7qcu0 anopheles g
1272	95.5	4.6	727	2	PECI_MOUSE	peci_mouse

No.	%		Len	n	Accession	Accession2	Organism	No.	%		Len	n	Accession	Accession2	Organism
1273	95.5	4.6	808	2	Q7PVZ3	Q7pvz3	anopheles g	1346	94	4.5	583	2	Q8VZR7	Q8vzr7	arabidopsis
1274	95.5	4.6	816	2	Q8IYD7	Q8iyd7	homo sapien	1347	94	4.5	602	2	Q9VFD9	Q9vfd9	drosophila
1275	95.5	4.6	879	2	Q8VI99	Q8vi99	rattus norv	1348	94	4.5	943	2	O30320	O30320	archaeoglob
1276	95.5	4.6	887	2	Q8YWI7	Q8ywi7	anabaena sp	1349	94	4.5	1010	1	CONT_CHICK	P14781	gallus gall
1277	95.5	4.6	888	2	Q8VIA0	Q8via0	rattus norv	1350	94	4.5	1280	2	Q9EPX2	Q9epx2	mus musculu
1278	95.5	4.6	1131	1	MYPF_CHICK	P16419	gallus gall	1351	94	4.5	1325	1	YDEK_ECOLI	P32051	escherichia
1279	95.5	4.6	1163	2	Q94HM5	Q94hm5	oryza sativ	1352	94	4.5	1406	2	Q9GPP7	Q9gpp7	drosophila
1280	95.5	4.6	1163	2	Q7XGI9	Q7xgi9	oryza sativ	1353	94	4.5	1463	2	Q9VQ08	Q9vq08	drosophila
1281	95.5	4.6	1242	1	NPHN_MOUSE	Q9QZS7	mus musculu	1354	94	4.5	1648	2	Q12275	Q12275	saccharomyc
1282	95.5	4.6	1264	2	Q91767	P91767	manduca sex	1355	94	4.5	1945	2	Q9V491	Q9v491	drosophila
1283	95.5	4.6	1948	1	PTNS_HUMAN	Q13332	homo sapien	1356	94	4.5	13133	2	Q71A42	Q71a42	caenorhabdi
1284	95.5	4.6	181	2	Q91665	Q91665	xenopus lae	1357	93.5	4.5	259	2	Q8UVA5	Q8uva5	brachydanio
1285	95	4.5	229	2	Q7PVL3	Q7pvl3	anopheles g	1358	93.5	4.5	261	2	Q8AUQ4	Q8auq4	brachydanio
1286	95	4.5	252	2	Q9CX63	Q9cx63	mus musculu	1359	93.5	4.5	296	2	O42404	O42404	gallus gall
1287	95	4.5	270	2	O00426	O00426	homo sapien	1360	93.5	4.5	313	2	Q8UV33	Q8uv33	brachydanio
1288	95	4.5	312	2	Q8BEJ3	Q8bej3	mus musculu	1361	93.5	4.5	315	2	Q6UN41	Q6un41	cowpox viru
1289	95	4.5	330	2	Q8C2J8	Q8c2j8	mus musculu	1362	93.5	4.5	326	2	Q8UV70	Q8uv70	brachydanio
1290	95	4.5	343	2	Q6U7R4	Q6u7r4	mus musculu	1363	93.5	4.5	330	1	CD86_RABIT	P42071	oryctolagus
1291	95	4.5	362	2	Q8CIC7	Q8cic7	mus musculu	1364	93.5	4.5	332	2	Q95L16	Q95l16	felis silve
1292	95	4.5	388	2	Q92151	Q92151	mus musculu	1365	93.5	4.5	332	2	Q9GMZ7	Q9gmz7	felis silve
1293	95	4.5	405	2	Q6PFK4	Q6pfk4	brachydanio	1366	93.5	4.5	336	2	Q8WVV5	Q8wvv5	homo sapien
1294	95	4.5	438	2	Q920C3	Q920c3	mus musculu	1367	93.5	4.5	379	2	Q9CWW1	Q9cww1	mus musculu
1295	95	4.5	457	2	Q96OD1	Q96od1	drosophila	1368	93.5	4.5	492	2	Q9ET54	Q9et54	mus musculu
1296	95	4.5	509	1	SHS1_RAT	P97710	rattus	1369	93.5	4.5	510	2	Q801V8	Q801v8	brachydanio
1297	95	4.5	521	1	C166_RABIT	O46651	oryctolagus	1370	93.5	4.5	655	2	Q8A9U5	Q8a9u5	bacteroides
1298	95	4.5	739	1	PECI_BOVIN	P51866	bos taurus	1371	93.5	4.5	729	1	FGR1_DROME	Q07407	drosophila
1299	95	4.5	814	2	Q8IVU1	Q8ivu1	homo sapien	1372	93.5	4.5	808	1	FGR4_MOUSE	Q03142	mus musculu
1300	95	4.5	814	2	Q91897	Q91897	xenopus lae	1373	93.5	4.5	853	2	Q6DFX7	Q6dfx7	xenopus lae
1301	95	4.5	847	2	Q8BFR2	Q8bfr2	m mus muscu	1374	93.5	4.5	1038	2	O42480	O42480	debaryomyce
1302	95	4.5	847	2	Q8C4T3	Q8c4t3	mus musculu	1375	93.5	4.5	1210	2	Q6BLQ0	Q6blq0	debaryomyce
1303	95	4.5	949	1	MDC1_MOUSE	P60755	mus musculu	1376	93.5	4.5	1264	2	O14631	O14631	homo sapien
1304	95	4.5	1052	2	Q7PMY4	Q7pmy4	anopheles g	1377	93.5	4.5	1630	2	Q90724	Q90724	gallus gall
1305	95	4.5	1371	2	Q8BV57	Q8bv57	mus musculu	1378	93.5	4.5	3396	1	PGCV_HUMAN	P13611	homo sapien
1306	95	4.5	1450	1	MPSF_CHICK	O02173	gallus gall	1379	93	4.5	280	2	Q8UV51	Q8uv51	brachydanio
1307	95	4.5	1501	2	Q7TT17	Q7tt17	mus musculu	1380	93	4.4	308	2	Q9ICI7	Q9ici7	vaccinia vi
1308	95	4.5	1501	2	Q9QW00	Q9qw00	rattus	1381	93	4.4	330	2	Q7PXA4	Q7pxa4	anopheles g
1309	95	4.5	1527	2	Q9VZZ4	Q9vzz4	drosophila	1382	93	4.4	333	2	Q9PZW8	Q9pzw8	homo sapien
1310	95	4.5	1863	2	O64605	O64605	rattus norv	1383	93	4.4	370	1	C244_HUMAN	C244_HUMAN	homo sapien
1311	95	4.5	1898	2	Q9EQ17	Q9eq17	mus musculu	1384	93	4.4	379	2	Q80UI9	Q80ui9	mus musculu
1312	95	4.5	1898	2	O64699	O64699	mus musculu	1385	93	4.4	388	1	BASI_RAT	P26453	rattus norv
1313	95	4.5	1945	2	O96681	O96681	drosophila	1386	93	4.4	390	2	O22096	O22096	caenorhabdi
1314	95	4.5	22152	2	Q8WXI7	Q8wxi7	homo sapien	1387	93	4.4	413	2	Q70BR2	Q70br2	anopheles g
1315	95	4.5	315	1	HEMA_VACCC	P20978	vaccinia vi	1388	93	4.4	424	1	Q6KDB4	Q6kdb4	escherichia
1316	95	4.5	341	2	Q819K3	Q819k3	branchiosto	1389	93	4.4	435	1	Q8FIX7	Q8fix7	escherichia
1317	94.5	4.5	371	2	Q6DCH5	Q6dch5	xenopus lae	1390	93	4.4	459	2	Q90304	Q90304	carassius a
1318	94.5	4.5	454	2	Q6MG97	Q6mg97	rattus norv	1391	93	4.4	555	1	C166_CARAU	C166_CARAU	rattus norv
1319	94.5	4.5	570	2	Q6GLY1	Q6gly1	xenopus lae	1392	93	4.4	589	2	O22096	O22096	caenorhabdi
1320	94.5	4.5	588	1	C166_CHICK	P42292	gallus gall	1393	93	4.4	598	1	Q8BIW7	Q8biw7	drosophila
1321	94.5	4.5	593	2	Q6INM5	Q6inm5	xenopus lae	1394	93	4.4	606	2	Q9B220	Q9b220	listeria mo
1322	94.5	4.5	733	2	Q902M7	Q902m7	mus musculu	1395	93	4.4	606	2	Q8BZD4	Q8bzd4	caenorhabdi
1323	94.5	4.5	755	2	Q8CCF8	Q8ccf8	mus musculu	1396	93	4.4	650	2	Q9GKR2	Q9gkr2	drosophila
1324	94.5	4.5	868	2	Q86VF2	Q86vf2	homo sapien	1397	93	4.4	719	2	Q8XA0	Q8xa0	bos taurus
1325	94.5	4.5	879	2	Q6PE80	Q6pe80	mus musculu	1398	93	4.4	736	2	Q8MYS2	Q8mys2	drosophila
1326	94.5	4.5	888	1	UFO_MOUSE	Q00993	mus musculu	1399	93	4.4	739	2	Q9GKR3	Q9gkr3	bos taurus
1327	94.5	4.5	888	2	Q80YQ3	Q80yq3	mus musculu	1400	93	4.4	739	2	Q8KOX1	Q8kox1	homo sapien
1328	94.5	4.5	931	1	UNSC_MOUSE	Q08747	mus musculu	1401	93	4.4	741	2	Q8KTF0	Q8ktf0	listeria mo
1329	94.5	4.5	999	1	MERK_HUMAN	Q12866	homo sapien	1402	93	4.4	774	2	Q9V930	Q9v930	drosophila
1330	94.5	4.5	1083	2	O76698	O76698	homo sapien	1403	93	4.4	831	2	Q70LU0	Q70lu0	bos taurus
1331	94.5	4.5	1327	2	VGR2_RAT	Q8QHL3	rattus norv	1404	93	4.4	841	2	O70LT9	O70lt9	homo sapien
1332	94.5	4.5	1343	1	Q80QH3	O08775	gallus gall	1405	93	4.4	848	2	Q28106	Q28106	bos taurus
1333	94.5	4.5	2425	2	Q95MJ0	Q95mj0	tupaia glis	1406	93	4.4	1018	2	Q28106	Q28106	bos taurus
1334	94.5	4.5	3029	2	Q7Q767	Q7q767	anopheles g	1407	93	4.4	1021	2	Q9P2X5	Q9p2x5	homo sapien
1335	94.5	4.5	252	2	Q86PE5	Q86pe5	drosophila	1408	93	4.4	1025	1	Q9H4E0	Q9h4e0	homo sapien
1336	94	4.5	275	2	Q7PVM4	Q7pvm4	anopheles g	1409	93	4.4	1094	2	P30315	P30315	plasmodium
1337	94	4.5	313	1	HEMA_VARV	P33807	variola vir	1410	93	4.4	1094	2	Q7KQI4	Q7kqi4	drosophila
1338	94	4.5	313	2	Q8AYW3	Q8ayw3	variola vir	1411	93	4.4	1310	2	Q96RV4	Q96rv4	homo sapien
1339	94	4.5	327	2	Q8BEI4	Q8bei4	variola vir	1412	93	4.4	1337	2	Q9BZA6	Q9bza6	homo sapien
1340	94	4.5	398	2	Q8UV63	Q8uv63	brachydanio	1413	93	4.4	1347	2	Q96RW0	Q96rw0	mus musculu
1341	94	4.5	419	2	Q723B9	Q723b9	homo sapien	1414	93	4.4	1347	2	Q9BZA7	Q9bza7	homo sapien
1342	94	4.5	484	2	Q86M56	Q86m56	drosophila	1415	93	4.4	2738	1	Qerb4	Qerb4	rattus norv
1343	94	4.5	533	2	Q99TQ8	Q99tq8	mus musculu	1416	93	4.4	3381	2	PGCV_RAT	P81282	bos taurus
1344	94	4.5	533	2	Q9DEE5	Q9dee5	gallus gall	1417	92.5	4.4	243	1	CAVT_BRALA	P05548	branchiosto
1345	94	4.5	583	2	O22889	O22889	arabidopsis	1418	92.5	4.4	245	1	MOG_RAT	Q63345	rattus norv

Seq	%	Val	Len	N	Accession / Name	Organism
1419	92.5	4.4	245	2	Q6MFX9	rattus norv
1420	92.5	4.4	277	2	Q6C6H8	mus musculu
1421	92.5	4.4	281	2	Q8CJE8	mesocricetu
1422	92.5	4.4	282	2	Q7Z7D3	homo sapien
1423	92.5	4.4	296	2	Q8WMZ2	sus scrofa
1424	92.5	4.4	310	2	Q8TQ07	methanosarc
1425	92.5	4.4	329	2	Q9XSX6	felis silve
1426	92.5	4.4	330	2	Q9Q242	gallus gall
1427	92.5	4.4	337	2	Q9VJF7	drosophila
1428	92.5	4.4	393	2	Q95727	homo sapien
1429	92.5	4.4	463	2	Q8C1V9	mus musculu
1430	92.5	4.4	474	2	Q8K178	mus musculu
1431	92.5	4.4	492	2	Q99KT6	mus musculu
1432	92.5	4.4	669	2	Q6NN86	drosophila
1433	92.5	4.4	762	2	Q71TW8	homo sapien
1434	92.5	4.4	763	2	Q9V1I4	drosophila
1435	92.5	4.4	764	1	Q8IZY7	homo sapien
1436	92.5	4.4	764	2	P01833 / PIGR_HUMAN	homo sapien
1437	92.5	4.4	821	1	Q63604 / TRKB_RAT	rattus norv
1438	92.5	4.4	886	2	Q9VM64	drosophila
1439	92.5	4.4	1053	2	Q6EQM4	oryza sativ
1440	92.5	4.4	1078	1	Q6NRQ4	xenopus lae
1441	92	4.4	222	2	Q8IX38	homo sapien
1442	92	4.4	290	2	Q7QCM3	anopheles g
1443	92	4.4	293	2	Q8AXN8	cyprinus ca
1444	92	4.4	305	2	Q98261	homo sapien
1445	92	4.4	305	2	Q8VBW0	mus musculu
1446	92	4.4	321	2	Q8MY16	ascaris suu
1447	92	4.4	323	1	Q08722 / CD47_HUMAN	homo sapien
1448	92	4.4	330	2	Q9N1E3	pongo pygma
1449	92	4.4	330	2	Q8C543 / CD22_PONPY	mus musculu
1450	92	4.4	367	2	Q6ZWL4	homo sapien
1451	92	4.4	419	2	Q68CR6	homo sapien
1452	92	4.4	422	2	Q7RTV9	homo sapien
1453	92	4.4	454	1	P01871 / MUC_HUMAN	homo sapien
1454	92	4.4	454	2	Q801W5	brachydanio
1455	92	4.4	485	2	Q8NG09	homo sapien
1456	92	4.4	526	2	Q7Z285	brachydanio
1457	92	4.4	544	2	Q90460 / C166_BRARE	brachydanio
1458	92	4.4	564	2	Q6IGX4 / C166_HUMAN	brachydanio
1459	92	4.4	583	2	Q13740	homo sapien
1460	92	4.4	607	2	Q80VF2	mus musculu
1461	92	4.4	613	2	Q96PQ0	homo sapien
1462	92	4.4	696	1	P59824 / IPL1_RAT	rattus norv
1463	92	4.4	696	2	Q9P244	homo sapien
1464	92	4.4	700	2	Q8C6V9	mus musculu
1465	92	4.4	738	2	Q7Q1P7	anopheles g
1466	92	4.4	826	2	Q8K0J1	mus musculu
1467	92	4.4	876	2	Q17576	caenorhabdi
1468	92	4.4	902	2	Q9B1Y1	caenorhabdi
1469	92	4.4	928	2	Q761X5 / UNSC_RAT	rattus norv
1470	92	4.4	931	1	Q9TTD7	trichosurus
1471	92	4.4	948	2	Q7Z553	homo sapien
1472	92	4.4	956	1	Q8C2F9 / MDC1_HUMAN	mus musculu
1473	92	4.4	1282	1	Q07113 / MPRI_MOUSE	mus musculu
1474	92	4.4	2483	1	P11717 / MPRI_HUMAN	homo sapien
1475	92	4.4	2491	1	Q96PT5	homo sapien
1476	92	4.4	2491	2	Q7Z7G9	homo sapien
1477	92	4.4	2491	2	Q8MQ08	caenorhabdi
1478	92	4.4	13100	2	Q09165	caenorhabdi
1479	91.5	4.4	153	2	Q9R1A2	mus musculu
1480	91.5	4.4	196	2	Q7PJY5	anopheles g
1481	91.5	4.4	234	2	Q6N895	homo sapien
1482	91.5	4.4	240	1	P18181 / CD48_MOUSE	mus musculu
1483	91.5	4.4	299	2	Q6P905	mus musculu
1484	91.5	4.4	366	2	Q9VHQ8	drosophila
1485	91.5	4.4	412	2	Q64216	spalax zemn
1486	91.5	4.4	451	2	Q8HXT9	tolypeutes
1487	91.5	4.4	459	2	Q8VD31	mus musculu
1488	91.5	4.4	459	2	Q86X91	homo sapien
1489	91.5	4.4	463	2	Q9GMB5	bos indicus
1490	91.5	4.4	541	2	Q95XJ7	caenorhabdi
1491	91.5	4.4	570	2	Q8NCE6	homo sapien
1492	91.5	4.4	573	2	Q8C6P3	mus musculu
1493	91.5	4.4	576	2	Q8C833	mus musculu
1494	91.5	4.4	576	1	P13504 / IL1R_MOUSE	mus musculu
1495	91.5	4.4	603	2	Q8VBZ9	mus musculu
1496	91.5	4.4	627	2	Q72PX7	leptospira
1497	91.5	4.4	675	2	Q7TOV5	xenopus lae
1498	91.5	4.4	789	2	Q8N2P7	homo sapien
1499	91.5	4.4	880	2	Q8QFP9	xenopus lae
1500	91.5	4.4	906	2	Q8UVU1	xenopus lae

RESULT 1

Q9Y279

ID	Q9Y279 PRELIMINARY; PRT; 399 AA.
AC	Q9Y279;
DT	01-NOV-1999 (TrEMBLrel. 12, Created)
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE	Z39Ig protein precursor (V-set and immunoglobulin domain containing
DE	4).
GN	Name=Z39Ig; Synonyms=VSIG4;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20461865; PubMed=11004523; DOI=10.1016/S0167-4781(00)00131-7;
RA	Langnaese K., Colleaux L., Kloos D.U., Fontes M., Wieacker P.;
RT	"Cloning of Z39Ig, a novel gene with immunoglobulin-like domains
RT	located on human chromosome X.";
RL	Biochim. Biophys. Acta 1492:522-525(2000).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RA	Director MGC Project;
RT	TISSUE=Brain;
RL	Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AJ132502; CAB51536.1; -.
DR	EMBL; BC010525; AAH10525.1; -.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003598; Ig_c2.
DR	Pfam; PF00047; ig; 1.
DR	SMART; SM00408; IGc2; 1.
DR	PROSITE; PS50835; IG_LIKE; 2.
KW	Signal.
FT	SIGNAL 1 19 Potential.

ALIGNMENTS

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FT   CHAIN        20     399
SQ   SEQUENCE   399 AA;  43987 MW;  291g protein.  735CA3BC58185035 CRC64;

Query Match
Best Local Similarity   100.0%;   Score 2098;   DB 2;   Length 399;
Matches 399;  Conservative 0;  Pred. No. 4.5e-157;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1  MGILLGLILLIGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MGILLGLILLIGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR  60

Qy   61  GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP  120

Qy  121  DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy  181  QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK  240

Qy  241  TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIIISLCCMVVFT   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIIISLCCMVVFT   300

Qy  301  MAYIMLCRKTSQQEHVEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE   360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  MAYIMLCRKTSQQEHVEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE   360

Qy  361  PCIGQOEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC  399
         ||||||||||||||||||||||||||||||||||||||||
Db  361  PCIGQOEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC  399
```

RESULT 2
Q6UXI4

```
ID   Q6UXI4            PRELIMINARY;     PRT;   321 AA.
AC   Q6UXI4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   STIGMA.
GN   ORFNames=UNQ317;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
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RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.,
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; AY358341; AAQ88707.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
```

```
SQ   SEQUENCE   321 AA;  35544 MW;  B2AB2B315ID39C6E CRC64;

Query Match
Best Local Similarity   80.5%;   Score 1688;   DB 2;   Length 321;
Matches 321;  Conservative 0;  Pred. No. 7.5e-125;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1  MGILLGLILLIGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MGILLGLILLIGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR  60

Qy   61  GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP  120

Qy  121  DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy  181  QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK  240

Qy  241  TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIIISLCCMVVFT   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIIISLCCMVVFT   300

Qy  301  MAYIMLCRKTSQQEHVEAAR  321
         ||||||||||||||||||||
Db  301  MAYIMLCRKTSQQEHVEAAR  321
```

RESULT 3
Q80WA3

```
ID   Q80WA3            PRELIMINARY;     PRT;   280 AA.
AC   Q80WA3;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein BC025105.
GN   Name=BC025105;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
```

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RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Liver;
```

SQ   SEQUENCE   280 AA;   31467 MW;   3F099A899GCE8977 CRC64;
KW   Hypothetical protein; IG_LIKE; 1.
DR   PROSITE; PS50835; IG_LIKE.
DR   InterPro; IPR007110; Ig-like.
DR   MGD; MGI:2679720; BC025105.
DR   EMBL; BC025105; AAH25105.1; -.
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RA   Strausberg R.;

Query Match   40.0%;   Score 840;   DB 2;   Length 280;
Best Local Similarity   47.4%;   Pred. No. 5e-58;
Matches 175;   Conservative 37;   Mismatches 57;   Indels 100;   Gaps 3;

```
Qy     1 MGILLGLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR   60
           ||  ||| ||||  || |||| ||||||| ||||| | ||||  || |||||||||| |
Db     1 MEISSGLLFLGHLILVLTYGHPTLKTPESVTGTWKGDVKIQCIYDPLRGYRQVLVKWLVRH  60

Qy    61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP  120
           |||.||||||||.||||||||| |||.|||||||||||| .||.||||.||||||||||
Db    61 GSDSVTIFLRDSTGDHIQQAKYRGRLKVSHKVPGDVSLQINTLQMDDRNHYTCEVTWQTP  120

Qy   121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQCMRISLQCQARGSPISYIWYKQ   180
           |||||.|.|| |||.||                              NPP
Db   121 DGNQVIRKIIELRVRKY------------------------------NPP---------  141

Qy   181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKQGVGSEQHSDIVKFVVKDSSKLLKTK  240
                                                                 RIN
Db   142 ------------------------------------------------------RIN  144

Qy   241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIIISLCCMVVFT  300
           ||||||..  ||.|   :|  :|   |||:||::::| |:.||:|||||:|||||||:|.||
Db   145 TEAPTTLHSSLEATTIMSSTSDLITNGTGKLEBTIAGSGRNLPIFAIIFIISLCCIVAVT  204

Qy   301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE  360
           :.|:.|.|:|.QQE|VY... |..:.           :..:  :|SD:::     :YSD:
Db   205 IPYILFRCRTFQQEYVYGVSRVPFARKTSNSEETRVTTIA----TDEPDSQALISDYSDD  260

Qy   361 PCIGQEYQI  369
           ||:.QEYQI
Db   261 PCUSQEYQI  269
```

RESULT 4
JAM1_HUMAN
ID   JAM1_HUMAN   STANDARD;   PRT;   299 AA.
AC   Q9Y624;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Junctional adhesion molecule 1 precursor (JAM) (platelet adhesion
DE   molecule 1) (PAM-1) (platelet F11 receptor) (UNQ264/PRO301).
GN   Name=F11R; Synonyms=JAM, JCAM;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99323940; PubMed=10395639;
RA   Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA   Iwamatsu A., Kita T.;
RT   "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
RT   of junctional adhesion molecule in human endothelial cells.";
RL   J. Immunol. 163:553-557(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss C.,
RA   Kornecki E.;
RT   "Molecular cloning and sequencing of the cDNA of F11 receptor, a novel
RT   Ig superfamily member from human platelets.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Naik U.P., Naik M.U., DeLeon P., Spychala J.;
RT   "Cloning and characterization of PAM-1, a novel platelet adhesion
RT   molecule involved in platelet activation.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
RA   Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA   Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
RA   Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA   Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA   Wambutt R., Korn B., Klein M., Poustka A.;
RT   "Towards a catalog of human genes and proteins: sequencing and
RT   analysis of 500 novel complete protein coding human cDNAs.";
RL   Genome Res. 11:422-435(2001).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22875296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P., Gray A.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [7]
RP   SEQUENCE OF 28-42.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
CC   -!- FUNCTION: Seems to plays a role in epithelial tight junction
CC   formation. Appears early in primordial forms of cell junction
CC   formation and recruits PARD3. The association of the PARD6-PARD3 complex may
CC   prevent the interaction of PARD3 with JAM1, thereby preventing
CC   tight junction assembly (By similarity). Plays a role in
CC   regulating monocyte transmigration involved in integrity of
CC   epithelial barrier. Involved in platelet activation (By
CC   similarity).
CC   -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC   association between PARD3 and PARD6B probably disrupts this
CC   interaction (By similarity).

RESULT 5
ID   Q10465   PRELIMINARY;   PRT;   7962 AA.
AC   Q10465;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)

CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC   epithelial and endothelial cells.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   --
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; AF111713; AAD42050.1; -.
DR   EMBL; AF207907; AAF22829.1; -.
DR   EMBL; AF172398; AAD48877.1; -.
DR   EMBL; AL136649; CAB66584.1; -.
DR   EMBL; AY358896; AAQ89255.1; -.
DR   EMBL; BC001533; AAH01533.1; -.
DR   PIR; A59406; S56749.
DR   PDB; 1NBQ; X-ray; A/B=25-233.
DR   Genew; HGNC;14685; F11R.
DR   MIM; 605721; -.
DR   GO; GO:0005911; C:intercellular junction; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   3D-structure; Direct protein sequencing; Glycoprotein;
KW   Immunoglobulin domain; Repeat; Signal; Tight junction; Transmembrane.
FT   SIGNAL   1   27
FT   CHAIN   28   299
FT   DOMAIN   28   299   Extracellular (Potential).
FT   TRANSMEM   239   259   Potential.
FT   DOMAIN   260   299   Cytoplasmic (Potential).
FT   DOMAIN   28   125   Ig-like V-type 1.
FT   DOMAIN   135   228   Ig-like V-type 2.
FT   DISULFID   50   109   Potential.
FT   DISULFID   153   212   Potential.
FT   CARBOHYD   185   185   N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   299 AA; 32583 MW; D95DE2FEA23D2851 CRC64;

Query Match   8.5%; Score 178.5; DB 1; Length 299;
Best Local Similarity   26.5%; Conservative 36; Mismatches 93; Indels 51; Gaps 11;
Matches 65;

Qy   1 MGILLGLILLGHLITVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
           ||| || | | :| | ||| || :| || | |:|
Db   17 LAILLCSLALGSVTVHS-SEPEVRIPEN----NPVKLSCAY---SGFSSPRVEW---- 62

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK------VPGDVSLQLSTLEMDRSHYTCEV 115
                 ||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   63 -------KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTRB--DTGTYYTCMV 111

Qy   116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVVTTGSGYGFTVPQGMRISLQCQQAR-GSPPIS 174
                  :| |:| |||||| |||:| | | | | | | || :
Db   112 SEEGGNSYGEVKRLIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSE 163

Qy   175 YIWYK----OQTN-------NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSBQH 222
           || | | | | | | | ||||||| || |:|| |
Db   164 YTWFKDGIVMPFNPKSTRAFSNSSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT 223

Qy   223 SDIVK 227
           :|::|
Db   224 SNAVR 228

RESULT 6
ID   Q8WZ42   PRELIMINARY;   PRT;   34350 AA.
AC   Q8WZ42;
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Elastic titin (Fragment).
DE   Name=titin;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RL   Science 270:293-296(1995).
RX   MEDLINE=96026330; PubMed=7569978;
RA   Labeit S., Kolmerer B.;
RT   "Titins: giant proteins in charge of muscle ultrastructure and
RT   elasticity.";
DR   EMBL; X90569; CAA62189.1; -.
DR   PIR; I38346; I38346.
DR   HSSP; P11362; 1EVT.
DR   GO; GO:0030017; C:sarcomere; TAS.
DR   GO; GO:0008307; F:structural constituent of muscle; TAS.
DR   GO; GO:0006941; P:striated muscle contraction; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_C2.
DR   InterPro; IPR004168; PPAK_motif.
DR   Pfam; PF02818; PPAK; 53.
DR   SMART; SM00408; IGC2; 43.
DR   PROSITE; PS50835; IG_LIKE; 58.
FT   NON_TER   1   1
FT   NON_TER   7962   7962
SQ   SEQUENCE   7962 AA; 883018 MW; B85240533CBADE58 CRC64;

Query Match   8.5%; Score 178; DB 2; Length 7962;
Best Local Similarity   24.2%; Conservative 56; Mismatches 169; Indels 94; Gaps 20;
Matches 102;

Qy   16 DTYGRPILEVPES-VTGPWKGDVNLP-----CTYDPLQGYTQVLVKW-----LVQRGSDP 64
           || ||| :| | :| || | |: :
Db   860 DSSGALIVQEPPSFVTKPGSKDV-LPGSAVCLKSTFQGSTPLTIRWFKGNKELVSGGSCY 918

Qy   65 VTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTPDG-- 122
           |:| | | :||||| | | | | | | |
Db   919 IT--------------------KEALESSLELYLVKTSDSGTYVTCKVS-NVAGVE 953

Qy   123 ---NQVVRDKITELRVQKLSVSKPTVVTTGSGYGFTVPQGMRISLQCQQARGSPPISYIWYK 179
              | |||||||| ||||:| | | | | | | | | | | |
Db   954 CSANLFVKEPAT--FVEKLBPSQ----------LLKKGDATQLACKVTGTPPIKITWFA 1000

Qy   180 QQTNNQEPIK-----VATLSTLLFKPAVIADSGSYFCTAKGQVGSBQHSDIVKFVVKDSS 234
           | ||||| | | | | ||||||| || |:|| | |: |:
Db   1001 NDREIKESSKHRMSFVESTAVLRLITDVGIEDSGEYMCEAQNEAGSDHCSSIV--IVKESP 1058

Qy   235 -----KLLKTKTEAPTTMTYPLKATSTVKQSMDWTTDMDGYLGETSAGPGKSLPVFAII 288
                | | | | | | | | | | | | | | | | | |
Db   1059 YFTKEFKPIEVLKEYDVWLLAEVAGTPPFEITW-------FKDNTILRSGRKYKTFIQD 1110

Qy   289 LIISLCCM--VVFTMAYIMLCRKTSQQEHVEAARAHAREAN------DSGETMR--VAIF 339
            | | | | | | | | | | | | | | |
Db   1111 HLVSLQILKFVAADAGEYQCRVTNEVGSSICSARVTLREPPSPIKKIESTSSLRGGTAAF 1170

Qy   340 ASGCSSDEPTSQNLGNNYSDEPCIGQEYQIIAQINGNYARL-LDTVPLDYEFLATEGRKSV 398
           | | | | | | || | | | | | | | | | | |
Db   1171 QATLKGSLPITVTWLKD-SDE--ITEDDNIRMTFENNVASLYISGIEVKH----DGKYV 1222

Qy   399 C 399
           |
Db   1223 C 1223

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DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Titin.
GN   Name=TTN;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20309627; PubMed=10850961;
RA   Freiburg A., Trombitas K., Hell W., Cazorla O., Fougerousse F.,
RA   Centner T., Kolmerer B., Witt C., Beckmann J.S., Gregorio C.C.,
RA   Granzier H., Labeit S.;
RT   "Series of exon-skipping events in the elastic spring region of titin
RT   as the structural basis for myofibrillar elastic diversity.";
RL   Circ. Res. 86:1114-1121 (2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21573839; PubMed=11717165;
RA   Bang M.L., Centner T., Fornoff F., Geach A.J., Gotthardt M.,
RA   McNabb M., Witt C.C., Labeit D., Gregorio C.C., Granzier H.,
RA   Labeit S.;
RT   "The complete gene sequence of titin, expression of an unusual ~700
RT   kDa titin isoform and its interaction with obscurin identify a novel
RT   Z-line to I-band linking system.";
RL   Circ. Res. 89:1065-1072(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Centner S.B.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ277892; CAD12456.1; -.
DR   PDB; 1TNM; NMR; @=33480-33579.
DR   PDB; 1TNN; NMR; @=33480-33579.
DR   Genew; HGNC:12403; TTN.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain.. .; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0008307; F:structural constituent of muscle; IEA.
DR   GO; GO:0007517; P:muscle development; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   Pfam; PF00041; fn3; 132.
DR   Pfam; PF00047; ig; 3.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF02818; PPAK; 53.
DR   ProDom; PD000001; Proc_kinase; 1.
DR   SMART; SM00060; FN3; 132.
DR   SMART; SM00408; IGc2; 65.
DR   SMART; SM00409; IG; 132.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00931; FGGY_KINASES_1; UNKNOWN_1.
DR   PROSITE; PS50853; FN3; 132.
DR   PROSITE; PS50835; IG_LIKE; 143.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00435; PEROXIDASE_1; UNKNOWN_1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
SQ   SEQUENCE 34350 AA; 3816189 MW; 5B1120058A7CE58A CRC64;

Query Match        8.5%;  Score 178;  DB 2;  Length 34350;
Best Local Similarity  24.2%;
Matches  102;  Conservative  56;  Mismatches 169;  Indels  94;  Gaps  20;

Qy    16 DTYGRPILEVPES--VTGPWKGDVNLP-----CTYDPLQGYTQVLVKW------LVQRGSDP 64
            |:| :  | |: |  :|   |: |   :|:|  |  :| ||
Db  5122 DSSGALIVQEPPSFVTKPGSKDV-LPGSAVCLKSTFQGSTPLTIRWFKGNKELVSGGSCY 5180

Qy    65 VTIFLRDSSGDHIQQAKYQGRLHVSHKYVPGDVSLQLSTLEMDRSHYTCEVTWQTPDG-- 122
            |:|   :|:  |:  |:      :|  |:  |||:||::
Db  5181 IT-----------------KEALESSLELYLVKTSDSGTYTCKVS-NVAGGVE 5215

Qy   123 --NQVRDKITELRVQKLSVSKPTVTVTGSGYGFTVPQGMRISLQCQARGSPPISIYWYK 179
```

RESULT 7

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ID   A33_HUMAN     STANDARD;      PRT;   319 AA.
AC   Q99795;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Cell surface A33 antigen precursor (Glycoprotein A33).
GN   Name=GPA33;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Colon carcinoma;
RX   MEDLINE=97165045; PubMed=9012807; DOI=10.1073/pnas.94.2.469;
RA   Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
RA   Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
RA   Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
RA   Burgess A.W.;
RT   "The human A33 antigen is a transmembrane glycoprotein and a novel
RT   member of the immunoglobulin superfamily.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
RN   [2]
RP   POST-TRANSLATIONAL MODIFICATIONS.
RX   MEDLINE=97396159; PubMed=9245713; DOI=10.1006/bbrc.1997.6966;
RA   Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
RA   Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
RA   Simpson R.J.;
RT   "Characterization of posttranslational modifications of human A33
RT   antigen, a novel palmitoylated surface glycoprotein of human
RT   gastrointestinal epithelium.";
RL   Biochem. Biophys. Res. Commun. 236:682-686(1997).
CC   -!- FUNCTION: May play a role in cell-cell recognition and signaling.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in normal gastrointestinal
CC       epithelium and in 95% of colon cancers.
CC   -!- PTM: N-glycosylated, contains approximately 8 kDa of N-linked
CC       carbohydrate.
CC   -!- PTM: Palmitoylated.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
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```
Db  5216 CSANLFVKEPAT--FVEKLEPSQ-------------LLKKGDATQLACKVTGTPPIKITWFA 5262
            |:|  | |                          : :|  |    ||:|| |   |||| :
Qy   180 QQTNNQEPIK-----VAILSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSS 234

Db  5263 NDRRIKESSKHRMSFVESTAVLRLTDVGIEDSGEYMCEAQNEAGSDHCSSIV--IVKESP 5320
Qy   235 ------KLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAII 288

Db  5321 YFIKEFKPIEVLKEYDVNLLAEVAGTPPEITW-----FKDNTILRSGRKYKTFIQD 5372
Qy   289 LIISLLCCM-VVFTWAYIMLCRKTSQQEHYEAARAHAREAN---------DSGETMR--VAIF 339

Db  5373 HLVSLQILKFVAADAGEYQCRVTNEVGSSICSARVTLREPPSFIKKIESTSSLRGGTAAF 5432
Qy   340 ASGCCSSDEPTSQNLGNNYSDEPCIGQEYQIIAQINGNYARL-LDTVPLDYEFPLATEGKSV 398

Db  5433 QATLKGSLPITVTWLKD-SDE--ITEDDNIRMTFENNVASLYLSGIEVKH------DGKYV 5484
Qy   399 C 399

Db  5485 C 5485
```

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CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; U79725; AAC50957.1; -.
CC
DR HSSP; O88792; 1F97.
DR Genew; HGNC:4445; GPA33.
DR MIM; 602171; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Antigen; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin domain; Lipoprotein; Palmitate; Signal; Transmembrane.
FT SIGNAL   1   21
FT CHAIN   22   319   Cell surface A33 antigen.
FT DOMAIN   22   235   Extracellular (Potential).
FT TRANSMEM   236   256   Potential.
FT DOMAIN   257   319   Cytoplasmic (Potential).
FT DOMAIN   22   134   Ig-like V-type.
FT DOMAIN   140   227   Ig-like C2-type.
FT DOMAIN   258   261   Poly-Cys.
FT DISULFID   43   117   Potential.
FT DISULFID   146   222   Potential.
FT DISULFID   162   211   Potential.
FT CARBOHYD   112   112   N-linked (GlcNAc...).
FT CARBOHYD   200   200   N-linked (GlcNAc...) (Potential).
FT CARBOHYD   223   223   N-linked (GlcNAc...) (Potential).
SQ SEQUENCE   319 AA; 35632 MW; 9BFC7AAF45C2408E CRC64;

Query Match   8.4%; Score 177; DB 1; Length 319;
Best Local Similarity   27.5%;
Matches   64; Conservative 39; Mismatches 94; Indels 36; Gaps 11;

Qy   4 LIGLLLLGHLTVDTYGRPILEVPESVTGPWKG-DVNLPCTYDPLQGYTQVLVKW--LVQR 60
              :.||||::.|:::| ||. ||||.|| :||.|| :||::| ||:||||| |||
Db   8 VLWTLCAVRVTVDAIS---VETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKLLLT 64

Qy   61 GSDPVTIFLRDSSGDHIQQAKXYQGRLHVSHKV-PGDVSLQLSTLEMDDRSHYTCEVTWQT 119
              |||||||||||||||| || |||||||||| ||||||:|| ||||||||||||.||:
Db   65 HTERVVIW-PFSNKNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMS 123

Qy   120 P-DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQAR-GSPPISYIW 177
              | |||| |||||||||||||| :| :| | ||:|:: |||||| :| ||||:||:|
Db   124 DLEGN------TKSRVRLLVLVPPSKPECGIEGETI-IGNNIQLICQSKEGSPTPQYSW 175

Qy   178 YKQQTNNQE--------------PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSE 220
              ||:|||:|: ||:|||||||||::| :|||||||| ||::|
Db   176 KRYNILNQEQPLAQPASGQPVSLKNIST------------DTSGYYICTSSNEEGTQ 220

RESULT 8
ID   Q66I72   PRELIMINARY;   PRT;   292 AA.
AC   Q66I72;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Zgc:103642.
GN   Name=zgc:103642.
OS   Brachydanio rerio (zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Larvae;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Larvae;
RA   Director MGC Project;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC081502; AAH81502.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_C2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   292 AA; 32091 MW; E1F6B5FE74A72502 CRC64;

Query Match   8.1%; Score 170.5; DB 2; Length 292;
Best Local Similarity   28.6%;
Matches   64; Conservative 25; Mismatches 94; Indels 41; Gaps 10;

Qy   28 SVTGPWK----GDVNLPCTYDPLQGYTQVLVKWLVQ--RGSDPVTIFLRDSSGDHIQQAK 81
              ||.||| . ||||||||. | :| |:|||||:||. |:|||||||||||||||||||
Db   22 TVTSPVKVKENEGVDLQCSYTSDFGATP-RVEWKFKDLKGSQTLVYF-----DGKPTCQ 74

Qy   82 YQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVS 141
              ::|||||:|| ||||||||||||||||||||||| || ||| ||||||||||||||
Db   75 YIGRVTMY-----DKGLRFNKVTRADIGDYDCEVSGSGSGYGENTI-------KLTVL 119

Qy   142 KPTVTTGSGYGFTVPQGMRISLQC-QARGSPPISYIWYKQQTN-NQBPIKVATLSTLLFK 199
              ||||| || |||:|: |||||| :|||:|| :|| ::|||. |.| || |:||.|||
Db   120 VPPAKPVSRIPSSVTTSSNVRLTCFDPVGSPPSTYKWYKDNTPLPEDPTKFPAPKNLTYK 179

Qy   200 -----------PAVI-ADSGSYFCTAKGQVGSEQHSDIVKFVVRD 232
                           |||| ||||||| || ||: ||:|| |::| |
Db   180 MNVFNGNLEFPSVSKMDTGSYFCEASNEGVPQRGDEVKMEVRD 223

RESULT 9
ID   Q8WMV3   PRELIMINARY;   PRT;   365 AA.
AC   Q8WMV3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Coxsackie virus and adenovirus receptor BCAR.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21547769; PubMed=11688979; DOI=10.1006/bbrc.2001.5851;
RA   Thoelen I., Keyaerts E., Lindberg M., Van Ranst M.;
RT   "Characterization of a cDNA encoding the bovine coxsackie and
RT   adenovirus receptor.";
RL   Biochem. Biophys. Res. Commun. 288:805-808(2001).
DR   EMBL; AY033651; AAK57804.1; -.

Left column

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DR   PIR; JC7780; JC7780.
DR   HSSP; P78310; 1KAC.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Receptor.
SQ   SEQUENCE   365 AA;  40153 MW;  36DE0B5DCF88CF9 CRC64;

Query Match             Best Local Similarity   24.7%;
                        Score 170;  DB 2;  Length 365;
Matches   86;  Conservative   40;  Mismatches  124;  Indels   98;  Gaps  17;

Qy    1 MGILLGLILLGHLTVDTYGRPILEVPESVTGPWKGD-VNLPCTY------DPLQGYTQV 52
Db    1 MELLLRFLLCGVADFTRGLSI-TTPEQMIEKARGETAYLPCKFTLGPEDQGPLD----- 54

Qy   53 LVKWLVQRGS----DPVIFLRDSSGDHIQQAKYQ---GRLHVSHK--VPGDVSLQLSTL 103
Db   55 -IEWLLSPADNQKVDQVILLY---SGDKIYDDYYQDLKGRVHFTSNDLKSGDASINVTNL 110

Qy  104 EMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQ----GM 159
Db  111 QLSDIGTYQCKVKKAPGVGNK---------KIQLTVLVKP---------SGIRCVDGSEEIGN 156

Qy  160 RISLQCQAR-GSPISYIWYKQQTNNQEP--IKVATLSTLLFKPAVIADSGSYFCTAKG 215
Db  157 DFKLKCEPKEGSLPLRYEWQKLSDSQKLPTSWLPEMTSPVISVKNASABYSGYTVCTVRN 216

Qy  216 QVDSEQHSDIVKFVVKDSSKLLKTKTEAPTMTYPLKATSTVKQOSWDWTTDMDGYLGETS 275
Db  217 RVGSDQ---------------------------CLLRLDVVPPSNR--------------AGTI 239

Qy  276 AGFGKSLPVFAIILIISLCCMVPFMAYIMLCRKTSQQEHVYEAAARAH 323
Db  240 AG-----AVIGTLLALVLIALIVP--------CCHKKRREEKYEKEVHH 275
```

CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC   epithelial and endothelial cells.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC   association between PARD3 and PARD6B probably disrupts this
CC   interaction (By similarity).
CC   -!- FUNCTION: Seems to play a role in epithelial tight junction
CC   formation. Appears early in primordial forms of cell junctions and
CC   recruits PARD3. The association of the PARD6-PARD3 complex may
CC   prevent the interaction of PARD3 with JAM1, thereby preventing
CC   tight junction assembly (By similarity). Plays a role in
CC   regulating monocyte transmigration involved in integrity of
CC   epithelial barrier. Involved in platelet activation.

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RESULT 10
ID   JAM1_BOVIN
     JAM1_BOVIN     STANDARD;      PRT;   298 AA.
AC   Q9XT56;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Junctional adhesion molecule 1 precursor (JAM).
GN   Name=F11R; Synonyms=JAM1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=913;
```
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99323940; PubMed=10395639;
RA   Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA   Iwamatsu A., Kita T.;
RT   "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
RT   of junctional adhesion molecule in human endothelial cells.";
RL   J. Immunol. 163:553-557(1999).

Middle / right column

CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.

```
DR   EMBL; AF111714; AAD42051.1; -.
DR   HSSP; Q9Y624; INBQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Glycoprotein; Immunoglobulin domain; Repeat; Signal; Tight junction;
KW   Transmembrane.

FT   SIGNAL        1     24       Potential.
FT   CHAIN        25    298       Junctional adhesion molecule 1.
FT   DOMAIN       25    237       Extracellular (Potential).
FT   TRANSMEM    238    258       Potential.
FT   DOMAIN      259    298       Cytoplasmic (Potential).
FT   DOMAIN       28    124       Ig-like V-type 1.
FT   DOMAIN      134    227       Ig-like V-type 2.
FT   DISULFID     49    108       Potential.
FT   DISULFID    152    211       Potential.
FT   CARBOHYD    184    184       N-linked (GlcNAc...) (Potential).
SQ   SEQUENCE   298 AA;  32456 MW;  714FE1C1714769A2 CRC64;

Query Match             Best Local Similarity   8.1%;
                        Score 169.5;  DB 1;  Length 298;
Matches   63;  Conservative   31;  Mismatches   88;  Indels   69;  Gaps  11;

Qy    3 ILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRG- 61
Db   18 MILCSLALGRGAVQIY-EPVVRVPEN----NPAKLSCSY---SGFSSPRVEWFTHGD 67

Qy   62 ------SDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCE 114
Db   68 IRGLLVCYNNKIT----------ASYENRVTFS----DTGIFFHSVTRKDTGMYTCM 109

Qy  115 VTWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQAR-GSPPI 173
Db  110 VS----DEGGNTYGEVTVQLIVLVPPSKPTINVPS---SVTIGTRAVLTCSERDGSPPS 161

Qy  174 SYIWYK--------QQTNNQEPIKVATLSTLLFKPAVIADSGSYPCTAKG 215
Db  162 EYKWFKDGVEMPLEPKSNRAFSNSSYTLNQK------TGELIFPDVSASDTGDFTCQAQN 215

Qy  216 QVGSEQHSDIV 226
Db  216 GYASPVKSDTV 226
```

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RESULT 11
ID   Q8VC39
     Q8VC39         PRELIMINARY;   PRT;   300 AA.
AC   Q8VC39;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   F11r protein (Mus musculus adult male cecum cDNA, RIKEN full-length
DE   enriched library, clone:9130004G24 product:junction cell adhesion
DE   molecule1, full insert sequence).
GN   Name=F11r;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
```
RN   [1]
RP   SEQUENCE FROM N.A.

RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RG   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cecum;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cecum;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RG   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cecum;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RG   The FANTOM Consortium;
RG   The RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cecum;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]

RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cecum;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saito Y., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yaesunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC021876; AAH21876.1; -.
DR   EMBL; AK033574; BAC28369.1; -.
DR   HSSP; 088792; 1F97.
DR   MGD; MGI:1321398; Fllr.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   300 AA; 32423 MW; 3CE561E8FF3B97EC CRC64;

Query Match   8.0%; Score 168; DB 2; Length 300;
Best Local Similarity 24.8%; Pred. No. 5.6e-05;
Matches 75; Conservative 38; Mismatches 127; Indels 62; Gaps 14;

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Qy      3 ILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGS 62
            ::||| ||| ||  |    || ::::|  |  :||| |     |:   |   |  |  ||
Db     18 MILGSLVQGKGSVYT-AQSDVQVPENES-----IKLTCTY---SGFSSPRVEWKFVQGS 67

Qy     63 DPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDG 122
           |  | |||| |||  |   | |||   :     | |     ||  |: |||| |    ::
Db     68 TTALVCVNSQI-----TAPYADRVTFSSS-----GITFSSVTRKDNGEYTCMV---SEEG 114

Qy    123 NQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQAR-GSPPISYIWYKQQ 181
           | |  |:| | |  |:       | |  |  :  :|||| ||| |  |:| || | |||
Db    115 GQNYGEVSIHLTV-LVPPSKPTISVPS---SVTIGNRAVLTCSEHDGSPPSEYSWFK--- 167

Qy    182 TNNQEPIKVATLST---------------LLFKPAVIADSGSYFCTAKGQVGSEQH 222
                 | | || ||                ||| | |  ||| |::  | | ||  |
Db    168 ----DGISMLTADAKKTRAFMNSSFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMR 223

Qy    223 SDIVKFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAG---PGK 280
           | |  | |||  || ||| |||  | :| ||  |  ::||| |  ||:| ||  |   |
Db    224 SEAAHM----DAVELNVGGIVAAVLVTLILLGLLIFGV---WPAYSRGYFPRTKKGTAPGK 277

Qy    281 SL 282
           :
Db    278 KV 279
```

RESULT 12
Q9TU79

ID   Q9TU79   PRELIMINARY;   PRT;   319 AA.
AC   Q9TU79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Coxsackie-adenovirus-receptor homolog (Fragment).
GN   Name=CAR;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99422053; PubMed=10490761;
RC   TISSUE=Liver;
RA   Fechner H., Haack A., Wang H., Wang X., Eizema K., Pauschinger M.,

RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultheiss H.P.,
RA Lamers J.M.J., Poller W.;
RT "Expression of Coxsackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers.";
RL Gene Ther. 6:1520-1535(1999).
DR EMBL; AF109646; AAF01257.1; -.
DR HSSP; P78310; 1KAC.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
FT NON_TER   319   319
SQ SEQUENCE   319 AA;   35301 MW; C4B5555A6C9F1B5B CRC64;

Query Match   8.0%;   Score 168; DB 2;   Length 319;
Best Local Similarity   24.1%; Pred. No. 6.1e-05;
Matches 83; Conservative 44; Mismatches 127; Indels 90;   Gaps 16;

Qy   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGD-VNLPCTY------DPLQGYTQV 52
           : :: ||| ::::|::||:||| | || | :| :| | || | | ||
Db   1 MALLREVLLCGV-ADLTRSLSITTPEQMIEKAKGETAYLPCKRFTLGPEDQGPLD---- 54

Qy   53 LVXWLVQRGS-----DPVTIFLRDSSGDHIQQAKYQ---GRLHVSHK--VPGDVSLQLSTL 103
           || ||||| || | | | | | | | || | | || | | |
Db   55 -IEWLLSPADNQKVDQVILY---SGDKIYDDYQDLKGRVHFTSNDLKSGDASINVTNL 110

Qy   104 EMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISL 163
           | || ||| || || | |||| || |||| : | | | | | |
Db   111 QLSDIGTYQCKVKAPGVGNK-------KIQLTVLLKPSGTRCYVDG-SEEIGNDFKL 160

Qy   164 QCQAR-GSPPISYIWYKQQTNNQEP---IKVATLSTLLFKPAVIADSGSYFCTAKGQVGS 219
           | | | || || | || | | | | | ||||| | |||| | | |
Db   161 KCEPKEGSLPLLYEWQKLSNSQKLPTLWLAEMTSPVISVKNASTEYSGTYSCTVKNRVGS 220

Qy   220 EQHSDIVKFVVKDSSKLLKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPG 279
           | | || | | ||| |||| || | :| | | || | ||| | | | |
Db   221 DQ--------CLLRLDVVPPSNR---------------------AGTIAG-- 241

Qy   280 KSLPVFAIILIISLCCMVVFTMAYIMLCRKTSQQEHVYEAARAH 323
           |||||| |:|::|| ||| |||| :| |||||||||||| |: :
Db   242 --AVIGVLLALVLIGLIVF------------CCHKKREEKYEKEVHH 275

RESULT 13
ID Q9TU80
AC Q9TU80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Coxsackie-adenovirus-receptor homolog (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=breed German shepherd; TISSUE=Liver;
RX MEDLINE=99422053; PubMed=10490761;
RA Fechner H., Haack A., Wang X., Pauschinger M.,
RA Schoemaker R.G., van Veghel R., Houtsmuller A.B., Schultheiss H.-P.,
RA Lamers J.M.J., Poller W.;
RT "Expression of Coxsackie-adenovirus-receptor and alpha v-integrin does
RT not correlate with adenovector targeting in vivo indicating anatomical
RT vector barriers.";
RL Gene Ther. 6:1520-1535(1999).
DR EMBL; AF109645; AAF01256.1; -.
DR HSSP; P78310; 1EAJ.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_c2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Receptor.
FT NON_TER   319   319
SQ SEQUENCE   319 AA;   35422 MW; 85C63A5EC7986965 CRC64;

Query Match   8.0%;   Score 167.5; DB 2;   Length 319;
Best Local Similarity   24.4%; Pred. No. 6.7e-05;
Matches 86; Conservative 41; Mismatches 126; Indels 99;   Gaps 18;

Qy   1 MGILLGLLLLGHLTVDTYGRPI-LEVPESVTGPWKGD-VNLPCTY------DPLQGYTQ 51
           : :: ||| ::::|::||:|| | || | :| :| | || | | ||
Db   1 MALLREVLLL--CGVADFTRSLSITTPEQMIEKAKGETAYLPCKRFTLSPEDQGPLD---- 54

Qy   52 VLVXWLVQRGS-----DPVTIFLRDSSGDHIQQAKYQ---GRLHVSHK--VPGDVSLQLST 102
           | || ||||| || | | | | | | | || | | || | |
Db   55 --IEWLLSPADNQKVDQVILY---SGDKIYDDYQDLKGRVHFTSNDLKSGDASINVTN 109

Qy   103 LEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISL 162
           || || ||| || || | |||| || |||| : | | | | | |
Db   110 LRLSDIGTYQCKVKAPGVGNK-------KIQLTVLVKP-----SGIRCYVDGSYFPCTAK 158

Qy   156 MRISLQCQAR-GSPPISYIWYKQQTNNQEPIKVATLST---LLFKPAVIADSGSYFCTAK 214
           | | | | | || || | || | | | | | ||||| | |||| |
Db   159 NDFKLKCEPKEGSLPLQYEWQKLSNSQKTPSWSTDMTSPVISIKNASTEYSGTYVICTVT 215

Qy   215 GQVGSEQHSDIVKFVVKDSSKLLKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGET 274
           | | | | || | | ||| |||| || | :| | | || | ||| | |
Db   216 NRVSSDQCQ----------LRLNVVPPSNR-------------------AGT 238

Qy   275 SAGPCKSLPVFAIILIISLCCMVVFTMAYIMLCRKTSQQEHVYEAARAHARE 326
           | | | |||||| |:|::|| ||| |||| :| |||||||||||| |: :
Db   239 IAG-----AVVGILLALVLIGFIVF------------CCRKKREEKYEKEVHHDIRE 279

RESULT 14
ID JAM1_MOUSE   STANDARD;   PRT;   300 AA.
AC O88792;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Junctional adhesion molecule 1 precursor (JAM).
GN Name=F11r; Synonyms=Jam1, Jcam, Jcam1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98327120; PubMed=9660867; DOI=10.1083/jcb.142.1.117;
RA Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
RA Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
RA Simmons D., Dejana E.;
RT "Junctional adhesion molecule, a novel member of the immunoglobulin
RT superfamily that distributes at intercellular junctions and modulates
RT monocyte transmigration.";
RL J. Cell Biol. 142:117-127(1998).
RN [2]
RP INTERACTION WITH PARD3.
RX MEDLINE=21340266; PubMed=11447115; DOI=10.1093/emboj/20.14.3738;
RA Ebnet K., Suzuki A., Horikoshi Y., Hirose T.,
RA Meyer zu Brickwedde M.-K., Ohno S., Vestweber D.;
RT "The cell polarity protein ASIP/PAR-3 directly associates with
RT junctional adhesion molecule (JAM).";
RL EMBO J. 20:3738-3748(2001).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 212-238.
RX MEDLINE=21391702; PubMed=11500366; DOI=10.1093/embo/20.16.4391;
RA Kostrewa D., Brockhaus M., D'Arcy A., Dale G.E., Nelboeck P.,
RA Schmid G., Mueller F., Bazzoni G., Dejana E., Bartfai T.,
RA Winkler F.K., Hennig M.;

```
RT   "X-ray structure of junctional adhesion molecule: structural basis for
RT   homophilic adhesion via a novel dimerization motif.";
RL   EMBO J. 20:4391-4398(2001).
CC   -!- FUNCTION: Seems to plays a role in epithelial tight junction
CC       formation. Appears early in primordial forms of cell junctions and
CC       recruits PARD3. The association of the PARD6-PARD3 complex may
CC       prevent the interaction of PARD3 with JAM1, thereby preventing
CC       tight junction assembly. Plays a role in regulating monocyte
CC       transmigration involved in integrity of epithelial barrier.
CC   -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC       association between PARD3 and PARD6B probably disrupts this
CC       interaction.
CC   -!- SUBUNIT: Involved in platelet activation.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC       Localized at tight junctions of both epithelial and endothelial
CC       cells.
CC   -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC       epithelial and endothelial cells.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   -----------------------------------------------------------------------
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DR   EMBL; U89915; AAC32982.1; -.
DR   PDB; 1F97; X-ray; A=27-238.
DR   MGD; MGI:1321398; F11r.
DR   GO; GO:0005515; F:protein binding; IPI.
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DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 2.
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DR   PROSITE; PS50835; IG_LIKE; 2.
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KW   Tight junction; Transmembrane.
FT   SIGNAL        1     26       Potential.
FT   CHAIN        27    300       Junctional adhesion molecule 1.
FT   DOMAIN       27    238       Extracellular (Potential).
FT   TRANSMEM    239    259       Potential.
FT   DOMAIN      260    299       Cytoplasmic (Potential).
FT   DOMAIN       28    122       Ig-like V-type 1.
FT   DOMAIN      134    230       Ig-like V-type 2.
FT   DISULFID     49    108       Potential.
FT   DISULFID    152    212       Potential.
FT   CARBOHYD     42     42       N-linked (GlcNAc...) (Potential).
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Qy  281 SL 282
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DE   Junctional adhesion molecule JAM (Junctional adhesion molecule
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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RC   STRAIN=Sprague Dawley;
RA   Mashima H., Kojima I.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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RC   TISSUE=Prostate;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA   Stapleton M.; Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
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RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RA   Strausberg R.;
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
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Search completed: March 2, 2005, 15:24:31
Job time : 112 secs

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: March 2, 2005, 15:13:50 ; Search time 56 Seconds
(without alignments)
2337.317 Million cell updates/sec

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Perfect score: 2098
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Scoring table: BLOSUM62
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Searched: 1385339 seqs, 328044528 residues

Total number of hits satisfying chosen parameters: 1385339

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Database :   Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	2098	100.0	399	15	US-10-211-462-225	Sequence 225, App
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939	158.5	7.6	373	10	US-09-989-726-503	Sequence 503,	Appl
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941	158.5	7.6	373	10	US-09-978-564A-59	Sequence 59,	Appl
942	158.5	7.6	373	10	US-09-997-172-503	Sequence 503,	Appl
943	158.5	7.6	373	10	US-09-990-726-503	Sequence 503,	Appl
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945	158.5	7.6	373	10	US-09-999-833A-59	Sequence 59,	Appl
946	158.5	7.6	373	10	US-09-997-601-503	Sequence 503,	Appl
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952	158.5	7.6	373	10	US-09-997-683-503	Sequence 503,	Appl
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955	158.5	7.6	373	10	US-09-997-440-503	Sequence 503,	Appl
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958	158.5	7.6	373	10	US-09-997-857-503	Sequence 503,	Appl
959	158.5	7.6	373	10	US-09-999-834A-59	Sequence 59,	Appl
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961	158.5	7.6	373	10	US-09-997-469-503	Sequence 503,	Appl
962	158.5	7.6	373	10	US-09-978-423A-59	Sequence 59,	Appl

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1461	158.5	7.6	373	14	US-10-125-805-388	Sequence 388, App
1462	158.5	7.6	373	14	US-10-013-922A-59	Sequence 59, Appl
1463	158.5	7.6	373	14	US-10-020-445A-59	Sequence 59, Appl
1464	158.5	7.6	373	14	US-10-013-924A-59	Sequence 59, Appl
1465	158.5	7.6	373	14	US-10-124-821-388	Sequence 388, App
1466	158.5	7.6	373	14	US-10-152-385-388	Sequence 388, App
1467	158.5	7.6	373	14	US-10-152-393-388	Sequence 388, App
1468	158.5	7.6	373	14	US-10-152-396-388	Sequence 388, App
1469	158.5	7.6	373	14	US-10-153-552-388	Sequence 388, App
1470	158.5	7.6	373	14	US-10-156-840-388	Sequence 388, App
1471	158.5	7.6	373	14	US-10-156-841-388	Sequence 388, App
1472	158.5	7.6	373	14	US-10-156-842-388	Sequence 388, App
1473	158.5	7.6	373	14	US-10-156-844-388	Sequence 388, App
1474	158.5	7.6	373	14	US-10-156-845-388	Sequence 388, App
1475	158.5	7.6	373	14	US-10-156-846-388	Sequence 388, App
1476	158.5	7.6	373	14	US-10-121-045-388	Sequence 388, App
1477	158.5	7.6	373	14	US-10-121-052-388	Sequence 388, App
1478	158.5	7.6	373	14	US-10-121-053-388	Sequence 388, App
1479	158.5	7.6	373	14	US-10-121-054-388	Sequence 388, App
1480	158.5	7.6	373	14	US-10-121-063-388	Sequence 388, App
1481	158.5	7.6	373	14	US-10-123-212-388	Sequence 388, App
1482	158.5	7.6	373	14	US-10-123-213-388	Sequence 388, App
1483	158.5	7.6	373	14	US-10-123-291-388	Sequence 388, App
1484	158.5	7.6	373	14	US-10-123-322-388	Sequence 388, App
1485	158.5	7.6	373	14	US-10-123-771-388	Sequence 388, App
1486	158.5	7.6	373	14	US-10-123-911-388	Sequence 388, App
1487	158.5	7.6	373	14	US-10-124-823-388	Sequence 388, App
1488	158.5	7.6	373	14	US-10-084A-59	Sequence 59, Appl
1489	158.5	7.6	373	14	US-10-017-085A-59	Sequence 59, Appl
1490	158.5	7.6	373	14	US-10-127-900A-388	Sequence 388, App
1491	158.5	7.6	373	14	US-10-127-85A-388	Sequence 388, App
1492	158.5	7.6	373	14	US-10-128-685A-388	Sequence 388, App
1493	158.5	7.6	373	14	US-10-131-820A-388	Sequence 388, App
1494	158.5	7.6	373	14	US-10-142-886-388	Sequence 388, App
1495	158.5	7.6	373	15	US-10-145-016A-59	Sequence 59, Appl
1496	158.5	7.6	373	15	US-10-145-08A-59	Sequence 59, Appl
1497	158.5	7.6	373	15	US-10-145-092A-59	Sequence 59, Appl
1498	158.5	7.6	373	15	US-10-805-667-59	Sequence 59, Appl
1499	158.5	7.6	373	15	US-10-805-667-59	Sequence 59, Appl
1500	158.5	7.6	373	17	US-10-805-667-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-833-245-1236
; Sequence 1236, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1236
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-1236

  Query Match   100.0%; Score 2098; DB 11; Length 399;
  Best Local Similarity   100.0%; Pred. No. 2.4e-179;
  Matches 399; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGILLGLILLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
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Db   1 MGILLGLILLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy   121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy   181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

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Db  181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVFFT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVFFT 300
Qy  301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360
Qy  361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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Db  361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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RESULT 2
US-09-833-245-123b
; Sequence 1237, Application US/09833245
; Publication No. US20040101341A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1237
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-1237

Query Match   100.0%; Score 2098; DB 11; Length 399;
Best Local Similarity   100.0%; Pred. No. 2.4e-179;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
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Db    1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
Qy  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
Qy  181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
Qy  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVFFT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVFFT 300
Qy  301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360
Qy  361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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Db  361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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RESULT 3
US-10-458-143-8
; Sequence 8, Application US/10458143
; Publication No. US20040099950A1
; GENERAL INFORMATION:
; APPLICANT: Garcia, Pablo D.
; TITLE OF INVENTION: SECRETED HUMAN PROTEINS
; FILE REFERENCE: 1571.003/200130.510
; CURRENT APPLICATION NUMBER: US/10/458,143
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: US/09/546,309
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-458-143-8

Query Match   100.0%; Score 2098; DB 15; Length 399;
Best Local Similarity   100.0%; Pred. No. 2.4e-179;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
Qy  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
Qy  181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
Qy  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVFFT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVFFT 300
Qy  301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360
Qy  361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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Db  361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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RESULT 4
US-10-211-462-225
; Sequence 225, Application US/10211462
; Publication No. US20040003495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynne, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
; FILE REFERENCE: 018501-0062000US
; CURRENT APPLICATION NUMBER: US/10/211,462
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
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;       PRIOR FILING DATE: 2001-08-03
;       PRIOR APPLICATION NUMBER: US 60/334,244
;       PRIOR FILING DATE: 2001-11-29
;       NUMBER OF SEQ ID NOS: 230
;       SOFTWARE: Patentin Ver. 2.1
;
;   SEQ ID NO 225
;       LENGTH: 399
;       TYPE: PRT
;       ORGANISM: Homo sapiens

US-10-211-462-225

Query Match             100.0%;  Score 2098;  DB 15;  Length 399;
Best Local Similarity   100.0%;  Pred. No. 2.4e-179;
Matches  399;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 MGILLGLLLIGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
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Db          1 MGILLGLLLIGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy         61 GSDPVTIFLRDSSGDHIQQAAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GSDPVTIFLRDSSGDHIQQAAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy        121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy        181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
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Db        181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy        241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIIISLCCMVVFT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIIISLCCMVVFT 300

Qy        301 MAYIMLCRKTSQQEHVYEAARAARAEANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360
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Db        301 MAYIMLCRKTSQQEHVYEAARAARAEANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360

Qy        361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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Db        361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399


RESULT 5
US-10-633-008-32
;  Sequence 32, Application US/10633008
;  Publication No. US20040120957A1
;  GENERAL INFORMATION:
;       APPLICANT: Ashkenazi, Avi J.
;       APPLICANT: Fong, Sherman
;       APPLICANT: Goddard, Audrey
;       APPLICANT: Gurney, Austin L.
;       APPLICANT: Napier, Mary A.
;       APPLICANT: Tumas, Daniel
;       APPLICANT: Wood, William I.
;       APPLICANT: Van Lookren, Menno
;       TITLE OF INVENTION: USE OF A33 ANTIGENS AND JAM-IT
;       FILE REFERENCE: 39766/010OP1
;       CURRENT APPLICATION NUMBER: US/10/633,008
;       CURRENT FILING DATE: 2003-07-31
;       PRIOR APPLICATION NUMBER: US/10/265,542
;       PRIOR FILING DATE: 2002-10-03
;       PRIOR APPLICATION NUMBER: PCT/US00/04414
;       PRIOR FILING DATE: 2000-02-22
;       PRIOR APPLICATION NUMBER: PCT/US00/14042
;       PRIOR FILING DATE: 2000-05-22
;       PRIOR APPLICATION NUMBER: PCT/US00/32678
;       PRIOR FILING DATE: 2000-12-01
;       PRIOR APPLICATION NUMBER: US/09/254,465
;       PRIOR FILING DATE: 1999-03-05
;       PRIOR APPLICATION NUMBER: PCT/US99/05028
;       PRIOR FILING DATE: 1999-03-08
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;       NUMBER OF SEQ ID NOS: 36
;       SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 32
;       LENGTH: 399
;       TYPE: PRT
;       ORGANISM: Homo sapiens

US-10-633-008-32

Query Match             100.0%;  Score 2098;  DB 16;  Length 399;
Best Local Similarity   100.0%;  Pred. No. 2.4e-179;
Matches  399;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 MGILLGLLLIGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
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Db          1 MGILLGLLLIGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy         61 GSDPVTIFLRDSSGDHIQQAAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GSDPVTIFLRDSSGDHIQQAAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy        121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy        181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy        241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIIISLCCMVVFT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIIISLCCMVVFT 300

Qy        301 MAYIMLCRKTSQQEHVYEAARAARAEANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 MAYIMLCRKTSQQEHVYEAARAARAEANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360

Qy        361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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Db        361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399


RESULT 6
US-10-656-269-42
;  Sequence 42, Application US/10656269
;  Publication No. US20040152105A1
;  GENERAL INFORMATION:
;       APPLICANT: Bachmann, Martin
;       APPLICANT: Vogt, Lorenz
;       TITLE OF INVENTION: Immune Modulatory Compounds and Methods
;       FILE REFERENCE: 1700.0390002
;       CURRENT APPLICATION NUMBER: US/10/656,269
;       CURRENT FILING DATE: 2003-09-08
;       PRIOR APPLICATION NUMBER: 60/408,233
;       PRIOR FILING DATE: 2002-09-06
;       PRIOR APPLICATION NUMBER: 60/449,583
;       PRIOR FILING DATE: 2003-02-26
;       NUMBER OF SEQ ID NOS: 50
;       SOFTWARE: Patentin version 3.2
;   SEQ ID NO 42
;       LENGTH: 399
;       TYPE: PRT
;       ORGANISM: homo sapiens

US-10-656-269-42

Query Match             100.0%;  Score 2098;  DB 16;  Length 399;
Best Local Similarity   100.0%;  Pred. No. 2.4e-179;
Matches  399;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 MGILLGLLLIGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
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Db          1 MGILLGLLLIGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy         61 GSDPVTIFLRDSSGDHIQQAAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
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RESULT 7
; US-09-978-295A-52
; Sequence 52, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
  APPLICANT: Ashkenazi, Avi
  APPLICANT: Baker Kevin P.
  APPLICANT: Botstein, David
  APPLICANT: Desnoyers, Luc
  APPLICANT: Eaton, Dan
  APPLICANT: Ferrara, Napoleon
  APPLICANT: Filvaroff, Ellen
  APPLICANT: Fong, Sherman
  APPLICANT: Gao, Wei-Qiang
  APPLICANT: Gerritsen, Mary E.
  APPLICANT: Gerber, Hanspeter
  APPLICANT: Goddard, Audrey
  APPLICANT: Godowski, Paul J.
  APPLICANT: Grimaldi, J. Christopher
  APPLICANT: Gurney, Austin L.
  APPLICANT: Hillan, Kenneth J
  APPLICANT: Kljavin, Ivar J.
  APPLICANT: Kuo, Sophia S.
  APPLICANT: Napier, Mary A.
  APPLICANT: Pan, James;
  APPLICANT: Paoni, Nicholas F.
  APPLICANT: Roy, Margaret Ann
  APPLICANT: Shelton, David L.
  APPLICANT: Stewart, Timothy A.
  APPLICANT: Tumas, Daniel
  APPLICANT: Williams, P. Mickey
  APPLICANT: Wood, William I.
  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
  TITLE OF INVENTION: Acids Encoding the Same
  FILE REFERENCE: P2630P1C11
  CURRENT APPLICATION NUMBER: US/09/978,295A
  CURRENT FILING DATE: 2001-10-15
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  PRIOR FILING DATE: 1997-10-17
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Qy     241  TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIIIISLCCMVVFT  300
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~ ; PRIOR FILING DATE: 1998-05-15

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RESULT 8
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~ ; Sequence 52, Application US/09978697
; Patent No. US2002016928A1
; GENERAL INFORMATION:
~   APPLICANT: Ashkenazi, Avi
~   APPLICANT: Baker Kevin P.
~   APPLICANT: Botstein, David
~   APPLICANT: Desnoyers, Luc
~   APPLICANT: Eaton, Dan
~   APPLICANT: Ferrara, Napoleon
~   APPLICANT: Filvaroff, Ellen
~   APPLICANT: Fong, Sherman
~   APPLICANT: Gao, Wei-Qiang
~   APPLICANT: Gerber, Hanspeter
~   APPLICANT: Gerritsen, Mary E.
~   APPLICANT: Goddard, Audrey
~   APPLICANT: Godowski, Paul J.
~   APPLICANT: Grimaldi, J. Christopher
~   APPLICANT: Gurney, Austin L.
~   APPLICANT: Hillan, Kenneth J
~   APPLICANT: Kljavin, Ivar J.
~   APPLICANT: Kuo, Sophia S.
~   APPLICANT: Napier, Mary A.
~   APPLICANT: Pan, James;
~   APPLICANT: Paoni, Nicholas F.
~   APPLICANT: Roy, Margaret Ann
~   APPLICANT: Shelton, David L.
~   APPLICANT: Stewart, Timothy A.
~   APPLICANT: Tumas, Daniel
~   APPLICANT: Williams, P. Mickey
~   APPLICANT: Wood, William I.
~   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
~   TITLE OF INVENTION: Acids Encoding the Same
~   FILE REFERENCE: P2630P1C27
~   CURRENT APPLICATION NUMBER: US/09/978,697

CURRENT FILING DATE: 2001-10-16
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
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; PRIOR FILING DATE: 1998-03-31
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; PRIOR FILING DATE: 1998-03-31
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; PRIOR FILING DATE: 1998-04-01
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; PRIOR FILING DATE: 1998-05-13
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.

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; PRIOR APPLICATION NUMBER: 60/085573
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
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Query Match          80.5%;  Score 1688;  DB 9;  Length 321;
Best Local Similarity 100.0%;  Pred. No. 1e-142;
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Qy    1 MGILLGLILLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLLVKWLYQR 60
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Db    1 MGILLGLILLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLLVKWLYQR 60

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
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Db   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGPTVPQGMRISLQCQQARGSPPISYIWYKQ 180
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Db  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGPTVPQGMRISLQCQQARGSPPISYIWYKQ 180

Qy  181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTRAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
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Db  181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTRAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy  241 TEAPTTMTYPLKAITSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIILISLCCMVVFT 300
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Db  241 TEAPTTMTYPLKAITSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIILISLCCMVVFT 300

Qy  301 MAVIMLCRKTSQQEHVEAAR 321
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RESULT 10
US-09-953-499-2
Sequence 2, Application US/09953499
Publication No. US20020182206A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
```

; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER:
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US/09/953,499
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US/09/254,465
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
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; ORGANISM: Homo sapiens
US-09-953-499-2

Query Match   80.5%;   Score 1688;   DB 9;   Length 321;
Best Local Similarity   100.0%;   Pred. No. 1e-142;
Matches 321;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy  181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKPFVVKDSSKLLKTK 240
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Qy  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300
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Db  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300

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RESULT 11
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; Sequence 52, Application US/0999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918,585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
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Query Match     80.5%;   Score 1688;  DB 9;   Length 321;
Best Local Similarity    100.0%;  Pred. No. 1e-142;
Matches  321;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  MGILLGLILLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR  60
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Db    1  MGILLGLILLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR  60

Qy   61  GSDEVTIFLRDSSGDHIQQAKYQGRLHVSHKPVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GSDEVTIFLRDSSGDHIQQAKYQGRLHVSHKPVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy  121  DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
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Db  121  DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy  181  QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
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Db  181  QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy  241  TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIIISLCCMVFFT 300
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Db  241  TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIIISLCCMVFFT 300

Qy  301  MAYIMLCRKTSQQEHVYEAAR 321
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Db  301  MAYIMLCRKTSQQEHVYEAAR 321
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Hillan, Kenneth J
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P3C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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;  PRIOR APPLICATION NUMBER: 60/085704
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697
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Query Match             80.5%;  Score 1688;  DB 10;  Length 321;
Best Local Similarity   100.0%;  Pred. No. 1e-142;
Matches  321;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1  MGILLGLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MGILLGLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR  60

Qy    61  GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP  120

Qy   121  DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ  180

Qy   181  QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK  240

Qy   241  TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT  300
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Db   241  TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT  300

Qy   301  MAYIMLCRKTSQQEHVYEAAR  321
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Db   301  MAYIMLCRKTSQQEHVYEAAR  321
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RESULT 13
US-09-978-608A-52
;  Sequence 52, Application US/09978608A
;  Publication No. US20030045462A1
;  GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT: Baker Kevin P.
;  APPLICANT: Botstein, David
;  APPLICANT: Desnoyers, Luc
;  APPLICANT: Eaton, Dan
;  APPLICANT: Ferrara, Napoleon
;  APPLICANT: Filvacoff, Ellen
;  APPLICANT: Fong, Sherman
;  APPLICANT: Gao, Wei-Qiang
;  APPLICANT: Gerber, Hanspeter
;  APPLICANT: Gerritsen, Mary E.
;  APPLICANT: Godowski, Paul J.
;  APPLICANT: Goddard, Audrey
;  APPLICANT: Grimaldi, J. Christopher
;  APPLICANT: Gurney, Austin L.
;  APPLICANT: Hillan, Kenneth J
;  APPLICANT: Kljavin, Ivar J.
;  APPLICANT: Kuc, Sophia S.
;  APPLICANT: Napier, Mary A.
;  APPLICANT: Pan, James;
;  APPLICANT: Paoni, Nicholas F.
;  APPLICANT: Roy, Margaret Ann
;  APPLICANT: Shelton, David L.
;  APPLICANT: Stewart, Timothy A.
;  APPLICANT: Tumas, Daniel
;  APPLICANT: Williams, P. Mickey
;  APPLICANT: Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION: Acids Encoding the Same
;  FILE REFERENCE: P2630P1C22
;  CURRENT APPLICATION NUMBER: US/09/978,608A
;  CURRENT FILING DATE: 2001-10-16
;  NUMBER OF SEQ ID NOS: 624
;  Prior Application removed - See File Wrapper or Palm
;  SEQ ID NO 52
;  LENGTH: 321
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-978-608A-52
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Query Match             80.5%;  Score 1688;  DB 10;  Length 321;
Best Local Similarity   100.0%;  Pred. No. 1e-142;
Matches  321;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1  MGILLGLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MGILLGLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR  60

Qy    61  GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP  120

Qy   121  DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ  180

Qy   181  QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK  240

Qy   241  TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT  300
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Db  241 TEAPTTMTYPLKAISTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300
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Qy  301 MAYIMLCRKTSQQEHVYEAAR 321
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Db  301 MAYIMLCRKTSQQEHVYEAAR 321
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RESULT 14
US-09-978-585A-52
; Sequence 52, Application US/0997858SA
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 52
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-52

Query Match   80.5%; Score 1688; DB 10;   Length 321;
Best Local Similarity   100.0%; Pred. No. 1e-142;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MGILLGILLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
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Db    1 MGILLGILLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
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Db   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy  121 DGNQVRDKITELRVQKLSVSKPTVTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
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Db  121 DGNQVRDKITELRVQKLSVSKPTVTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy  181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
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Db  181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
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Qy  241 TEAPTTMTYPLKAISTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300
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Db  241 TEAPTTMTYPLKAISTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300

Qy  301 MAYIMLCRKTSQQEHVYEAAR 321
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RESULT 15
US-09-978-191A-52
; Sequence 52, Application US/0997819SA
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
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Job time : 80 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: March 2, 2005, 15:20:52 ; Search time 489 Seconds
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Post-processing: Minimum Match 0%
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177	1547	73.7	305	36	US-11-002-790-63	Sequence 63, Appl
178	1547	73.7	305	32	US-10-664-358-1009	Sequence 1009, Ap
179	1547	73.7	305	35	US-10-964-263-6	Sequence 6, Appli
180	1547	73.7	306	36	US-11-001-793-9422	Sequence 9422, Ap
181	1547	73.7	306	26	US-10-062-548-63	Sequence 63, App
182	1547	73.7	306	35	US-10-918-446-63	Sequence 63, App
183	1547	73.7	306	36	US-11-002-754-63	Sequence 63, App
184	1547	73.7	306	36	US-11-002-755-63	Sequence 63, App
185	1547	73.7	306	32	US-11-002-790-63	Sequence 63, App
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189	870	41.5	175	37	US-60-098-206-6	Sequence 6, Appli
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193	840	40.0	280	35	US-10-964-263-8	Sequence 8, Appli
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195	738	35.2	143	21	US-09-724-676A-67204	Sequence 67204, A
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198	653	31.1	131	21	US-09-724-676A-67205	Sequence 67205, A
199	653	31.1	131	21	US-09-724-676A-67205	Sequence 67205, A
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203	624.5	29.8	139	37	US-10-170-205E-22636	Sequence 22636, A
204	613	29.2	188	32	US-10-452-680-16137	Sequence 16137, A
205	492	23.5	93	1	US-10-656-269-16	Sequence 16, Appl
206	423	20.2	91	27	PCT-US01-06475-21	Sequence 21, Appl
207	237	11.3	47	30	US-10-161-073-233	Sequence 233, App
208	182	8.7	367	30	US-10-425-115-299346	Sequence 299346, A
209	182	8.7	367	27	US-60-245-228-285	Sequence 285, App
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224	178.5	8.5	37	296	US-60-636-723-741	Sequence 741, App
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883	178.5	8.5	299	33	US-10-785-433-1	Sequence 1, Appli
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1500	158.5	7.6	373	27	US-10-127-849A-388	Sequence 388, App

RESULT 1

PCT-US00-31162A-63

Sequence 63, Application PC/TUS0031162A

; GENERAL INFORMATION:
;   APPLICANT: Human Genome Sciences, Inc.
;   TITLE OF INVENTION: 18 Human Secreted Proteins
;   FILE REFERENCE: PS17PCT
;   CURRENT APPLICATION NUMBER: PCT/US00/31162A
;   CURRENT FILING DATE: 2000-11-15
;   PRIOR APPLICATION NUMBER: 60/166,415
;   PRIOR FILING DATE: 1999-11-19
;   PRIOR APPLICATION NUMBER: 60/215,136
;   PRIOR FILING DATE: 2000-06-30
;   NUMBER OF SEQ ID NOS: 161
;   SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 63
;   LENGTH: 399
;   TYPE: PRT
;   ORGANISM: Homo sapiens

PCT-US00-31162A-63

Query Match   100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity   100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

ALIGNMENTS

RESULT 2
PCT-US00-31162A-85
Sequence 85, Application PC/TUS0031162A2

; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: 18 Human Secreted Proteins
; FILE REFERENCE: PS717PCT
; CURRENT APPLICATION NUMBER: PCT/US00/31162A2
; CURRENT FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 60/166,415
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/215,136
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 85
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-31162A-85

Query Match   100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity   100.0%; Pred. No. 2.6e-193;
Matches 399;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120

Qy   121 DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy   181 QTNNQEPIKVATLSTLLFKPAVIADSGSSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 QTNNQEPIKVATLSTLLFKPAVIADSGSSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy   241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVFT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVFT 300

Qy   301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360

Qy   361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
            |||||||||||||||||||||||||||||||||||||||
Db   361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399

RESULT 3
PCT-US01-11988-1236
Sequence 1236, Application PC/TUS0111988

; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: PCT/US01/11988
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 1236
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-11988-1236

Query Match   100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity   100.0%; Pred. No. 2.6e-193;
Matches 399;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120

Qy   121 DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy   181 QTNNQEPIKVATLSTLLFKPAVIADSGSSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 QTNNQEPIKVATLSTLLFKPAVIADSGSSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy   241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVFT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVFT 300

Qy   301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360

Qy   361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
            |||||||||||||||||||||||||||||||||||||||
Db   361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399

RESULT 4
PCT-US01-11988-1237
Sequence 1237, Application PC/TUS0111988

; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PS46PCT
CURRENT APPLICATION NUMBER: PCT/US01/11988
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1237
LENGTH: 399
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-11988-1237

Query Match   100.0%;   Score 2098;   DB 1;   Length 399;
Best Local Similarity   100.0%;   Pred. No. 2.6e-193;
Matches 399;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy    1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy  181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIILIISLCCMVVFT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIILIISLCCMVVFT 300

Qy  301 MAYIMLCRKTSQQEHVYEAARARAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 MAYIMLCRKTSQQEHVYEAARARAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360

Qy  361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
        |||||||||||||||||||||||||||||||||||||||
Db  361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
```

RESULT 5
PCT-US02-04915-225
Sequence 225, Application PC/TUS0204915
GENERAL INFORMATION:
APPLICANT: Murray, Richard
APPLICANT: Glynne, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Aziz, Natasha
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and Methods of Screening for Angiogenesis Modulators
FILE REFERENCE: 018501-00620DPC
CURRENT APPLICATION NUMBER: PCT/US02/04915
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 09/784,356
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/791,390
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: US 60/285,475
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/310,025
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/334,244
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 230
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 225
LENGTH: 399
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-04915-225

Query Match   100.0%;   Score 2098;   DB 1;   Length 399;
Best Local Similarity   100.0%;   Pred. No. 2.6e-193;
Matches 399;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy    1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy  181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIILIISLCCMVVFT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIILIISLCCMVVFT 300

Qy  301 MAYIMLCRKTSQQEHVYEAARARAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 MAYIMLCRKTSQQEHVYEAARARAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360

Qy  361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
        |||||||||||||||||||||||||||||||||||||||
Db  361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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RESULT 6
PCT-US02-08123-1434
Sequence 1434, Application PC/TUS0208123
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS904PCT
CURRENT APPLICATION NUMBER: PCT/US02/08123
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 2048
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1434
LENGTH: 399
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-08123-1434

Query Match   100.0%;   Score 2098;   DB 1;   Length 399;
Best Local Similarity   100.0%;   Pred. No. 2.6e-193;
Matches 399;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy    1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 7
PCT-US02-08124-592
; Sequence 592, Application PCT/US0208124
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS901PCT
; CURRENT APPLICATION NUMBER: PCT/US02/08124
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/331,287
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/306,171
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/277,340
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 857
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 592
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens

SEQ ID NO 592
PCT-US02-08124-592

Query Match   100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MGILLGLLLLGHLTVDTYGRPILEVPESSVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGILLGLLLLGHLTVDTYGRPILEVPESSVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120

Qy  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy  181 QTNNQEPIKVATLSTLLFKPAVIADSGSSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 QTNNQEPIKVATLSTLLFKPAVIADSGSSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIILIISLCCMVVFT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIILIISLCCMVVFT 300

Qy  301 MAYIMLCRKTSQQEHVYEAARARARAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 MAYIMLCRKTSQQEHVYEAARARARAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360

Qy  361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
        |||||||||||||||||||||||||||||||||||||||
Db  361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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RESULT 8
PCT-US02-08276-446
; Sequence 446, Application PCT/US0208276
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS906PCT
; CURRENT APPLICATION NUMBER: PCT/US02/08276
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/331,287
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/306,171
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/277,340
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 650
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 446
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens

SEQ ID NO 446
PCT-US02-08276-446

Query Match   100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MGILLGLLLLGHLTVDTYGRPILEVPESSVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGILLGLLLLGHLTVDTYGRPILEVPESSVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120

Qy  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy  181 QTNNQEPIKVATLSTLLFKPAVIADSGSSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 QTNNQEPIKVATLSTLLFKPAVIADSGSSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIILIISLCCMVVFT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIILIISLCCMVVFT 300

Qy  301 MAYIMLCRKTSQQEHVYEAARARARAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 MAYIMLCRKTSQQEHVYEAARARARAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360

Qy  361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
        |||||||||||||||||||||||||||||||||||||||
Db  361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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RESULT 9
PCT-US02-08277-931
; Sequence 931, Application PCT/US0208277
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS907PCT

CURRENT APPLICATION NUMBER: PCT/US02/08277
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 1357
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 931
LENGTH: 399
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-08277-931

Query Match   100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy  61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy 181 QTNNQEPIKVATLSTLLFKPAVIADSGSGYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 QTNNQEPIKVATLSTLLFKPAVIADSGSGYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy 241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300

Qy 301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360

Qy 361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
       |||||||||||||||||||||||||||||||||||||||
Db 361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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RESULT 10
PCT-US02-08278-1373
Sequence 1373, Application PC/TUS0208278
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS902PCT
CURRENT APPLICATION NUMBER: PCT/US02/08278
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 1988
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1373
LENGTH: 399
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-08278-1373

Query Match   100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy  61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy 181 QTNNQEPIKVATLSTLLFKPAVIADSGSGYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 QTNNQEPIKVATLSTLLFKPAVIADSGSGYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy 241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300

Qy 301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360

Qy 361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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Db 361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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RESULT 11
PCT-US02-09785-795
Sequence 795, Application PC/TUS0209785
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS905PCT
CURRENT APPLICATION NUMBER: PCT/US02/09785
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 1130
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 795
LENGTH: 399
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-09785-795

Query Match   100.0%; Score 2098; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.6e-193;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy  61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy 181 QTNNQEPIKVATLSTLLFKPAVIADSGSGYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 12
PCT-US03-31207-32
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; Sequence 32, Application PC/TUS0331207
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC;
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Van Lookren, Menno
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Use of A33 Antigens and Jam-It
; FILE REFERENCE: 39766-0100PCT
; CURRENT APPLICATION NUMBER: 2003-10-01
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 10/633,008
; PRIOR FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 10/265,542
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 32
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
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PCT-US03-31207-32

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Query Match        100.0%;   Score 2098;  DB 1;  Length 399;
Best Local Similarity  100.0%;  Pred. No. 2.6e-193;
Matches 399;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy  61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120

Qy 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy 181 QTNNQEPIKVATLSTLLFKPAVIADSGSSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 QTNNQEPIKVATLSTLLFKPAVIADSGSSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy 241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIIIISLCCMVVFT 300
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIIIISLCCMVVFT 300

Qy 301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360

Qy 361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
       |||||||||||||||||||||||||||||||||||||||
Db 361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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RESULT 13
PCT-US04-34163-319
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; Sequence 319, Application PC/TUS0434163
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Pauloski, Nicole
; APPLICANT: Taylor, Ian
; APPLICANT: Bigwood, Douglas
; TITLE OF INVENTION: GENE EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 5176
; CURRENT APPLICATION NUMBER: PCT/US04/34163
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/508,355
; PRIOR FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 400
; SOFTWARE: Patentin version 3.3
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; SEQ ID NO 319
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
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PCT-US04-34163-319

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Query Match        100.0%;   Score 2098;  DB 1;  Length 399;
Best Local Similarity  100.0%;  Pred. No. 2.6e-193;
Matches 399;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy  61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYVPGDVSLQLSTLEMDRSHYTCEVTWQTP 120

Qy 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy 181 QTNNQEPIKVATLSTLLFKPAVIADSGSSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 QTNNQEPIKVATLSTLLFKPAVIADSGSSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy 241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIIIISLCCMVVFT 300
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Db 241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIIIIISLCCMVVFT 300

Qy 301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360

Qy 361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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Db 361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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RESULT 14
US-09-546-309-8
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; Sequence 8, Application US/09546309
; GENERAL INFORMATION:
; APPLICANT: Garcia, Pablo D.
; TITLE OF INVENTION: SECRETED HUMAN PROTEINS
; FILE REFERENCE: 1571.003/200130.510
; CURRENT APPLICATION NUMBER: US/09/546,309
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 8
; LENGTH: 399
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-546-309-8

Query Match                100.0%;   Score 2098;  DB 19;  Length 399;
Best Local Similarity      100.0%;   Pred. No. 2.6e-193;
Matches 399;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy     61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKYPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy    121 DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCCQARGSPPISYIWYKQ 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCCQARGSPPISYIWYKQ 180

Qy    181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy    241 TEAPTTMTYPLKAITSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TEAPTTMTYPLKAITSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300

Qy    301 MAYIMLCRKTSQQEHVYEAARARAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MAYIMLCRKTSQQEHVYEAARARAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360

Qy    361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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Db    361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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RESULT 15
US-09-833-245-1236
Sequence 1236, Application US/09833245
GENERAL INFORMATION:
   APPLICANT: Human Genome Sciences, Inc.
   TITLE OF INVENTION: Albumin Fusion Proteins
   FILE REFERENCE: PF546PCT
   CURRENT APPLICATION NUMBER: US/09/833,245
   CURRENT FILING DATE: 2001-04-12
   PRIOR APPLICATION NUMBER: 60/229, 358
   PRIOR FILING DATE: 2000-04-12
   PRIOR APPLICATION NUMBER: 60/256, 931
   PRIOR FILING DATE: 2000-12-21
   PRIOR APPLICATION NUMBER: 60/199, 384
   PRIOR FILING DATE: 2000-04-25
   NUMBER OF SEQ ID NOS: 2267
   SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1236:
   LENGTH: 399
   TYPE: PRT
   ORGANISM: Homo sapiens
US-09-833-245-1236

Query Match   100.0%;   Score 2098; DB 23; Length 399;
Best Local Similarity   100.0%;   Pred. No. 2.6e-193;
Matches 399; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy      1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy     61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSILQLSTLEMDDRSHYTCEVTWQTP 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSILQLSTLEMDDRSHYTCEVTWQTP 120

Qy    121 DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCCQARGSPPISYIWYKQ 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 DGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCCQARGSPPISYIWYKQ 180

Qy    181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy    241 TEAPTTMTYPLKAITSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TEAPTTMTYPLKAITSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300

Qy    301 MAYIMLCRKTSQQEHVYEAARARAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360
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Db    301 MAYIMLCRKTSQQEHVYEAARARAREANDSGETMRVAIFASGCSSSDEPTSQNLGNNYSDE 360

Qy    361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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Db    361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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Search completed: March   2, 2005, 15:32:22
Job time : 510 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: March 2, 2005, 15:16:16 ; Search time 26 Seconds
(without alignments)
689.930 Million cell updates/sec

Title: US-10-633-008-32
Perfect Score: 2098
Sequence: 1 MGILGLILLGHLTVDTYGR..........LLDTVPLDYEFLATEGKSVC 399

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 181127 seqs, 44957854 residues

Total number of hits satisfying chosen parameters: 181127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :   Pending_Patents_AA_New:*
1: /cgn2_6/ptcdata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptcdata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptcdata/2/paa/US07_NEW_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1688	80.5	321	5	US-09-978-191C-52	Sequence 52, Appl
2	870	41.5	175	5	US-10-986-822-6	Sequence 6, Appli
3	178.5	8.5	335	6	US-10-523-834-330	Sequence 330, Appl
4	159	7.6	365	6	US-10-155-282B-11	Sequence 11, Appl
5	159	7.6	365	8	US-60-651-509-101	Sequence 101, App
6	159	7.6	365	8	US-60-651-509-103	Sequence 103, App
7	158.5	7.6	373	5	US-09-978-191C-59	Sequence 59, Appl
8	157.5	7.5	351	6	US-10-523-834-331	Sequence 331, Appl
9	156	7.4	737	6	US-10-523-834-32378	Sequence 32378, A
10	154.5	7.4	5622	1	PCT-US05-03380-128	Sequence 128, App
11	153.5	7.3	518	7	US-11-049-6397-2	Sequence 2, Appli
12	151	7.2	434	6	US-10-450-763-32476	Sequence 32476, A
13	146.5	7.0	361	6	US-10-450-763-52760	Sequence 52760, A
14	139.5	7.0	3707	6	US-10-852-335A-139	Sequence 139, A
15	139	6.6	545	1	PCT-US05-02350-272	Sequence 272, App
16	139	6.6	545	7	US-11-043-770-272	Sequence 272, App
17	139	6.6	1089	1	US-10-450-763-51112	Sequence 51112, A
18	139	6.6	1106	1	PCT-US05-02350-267	Sequence 267, App
19	139	6.6	1106	7	US-11-043-770-267	Sequence 267, App
20	138	6.6	236	6	US-10-450-763-53622	Sequence 53622, A
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22	138	6.6	1645	6	US-10-450-763-50367	Sequence 50367, A
23	138	6.6	1765	6	US-10-450-763-52990	Sequence 52990, A
24	138	6.6	1944	6	US-10-450-763-42376	Sequence 42376, A
25	137	6.5	981	6	US-10-450-763-52992	Sequence 52992, A
26	137	6.5	5266	6	US-10-450-763-38920	Sequence 38920, A
27	136	6.5	2993	6	US-10-450-763-54243	Sequence 54243, A
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32	130	6.2	4436	7	US-10-450-763-53624	Sequence 53624, A
33	126	6.0	1219	6	US-10-450-763-42459	Sequence 42459, A
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36	124	5.9	848	6	US-10-450-763-5160	Sequence 160, App
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39	123	5.8	336	5	US-60-651-509-445	Sequence 445, App
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45	120	5.7	316	6	US-10-499-352A-474	Sequence 474, App
46	120	5.7	810	6	US-10-499-352A-467	Sequence 467, App
47	120	5.7	316	6	US-10-499-352A-465	Sequence 465, App
48	120	5.7	921	6	US-10-499-352A-473	Sequence 473, App
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58	118	5.6	522	7	US-10-051-724-48	Sequence 48, Appl
59	118	5.6	686	6	US-10-051-724-50	Sequence 50, Appl
60	118	5.6	686	7	US-11-051-724-48	Sequence 48, Appl
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62	118	5.6	686	7	US-11-051-724-42	Sequence 42, Appl
63	118	5.6	961	7	US-11-051-724-42	Sequence 42, Appl
64	118	5.6	1300	7	US-11-051-724-30	Sequence 30, Appl
65	118	5.6	1338	7	PCT-US04-23166A-611	Sequence 611, App
66	118	5.6	1338	7	US-11-043-770-530	Sequence 530, App
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74	117	5.6	677	7	PCT-US05-02350-530	Sequence 530, App
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76	116.5	5.5	338	7	US-11-043-770-530	Sequence 530, App
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79	116	5.5	344	6	US-09-978-191C-137	Sequence 137, App
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90	112.5	5.4	445	7	US-11-043-591-110	Sequence 110, App
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92	112.5	5.4	539	7	US-11-043-591-114	Sequence 114, App
93	112.5	5.3	623	7	US-11-043-591-101	Sequence 101, App
94	112	5.3	832	1	US-11-043-591-107	Sequence 107, App
95	112	5.3	620	1	PCT-US05-04041-369	Sequence 369, App
96	111.5	5.3	1070	8	US-60-651-509-636	Sequence 636, App
97	111	5.3	252	8	US-60-651-509-102	Sequence 102, App
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102	110.5	5.3	544	7	US-09-978-191C-259	Sequence 259, App
103	110.5	5.3	544	6	US-10-184-644-118	Sequence 118, App
104	110.5	5.2	295	7	US-11-048-692-31	Sequence 31, Appl
105	109	5.2	445	6	US-10-450-763-40404	Sequence 40404, A
106	109	5.2	506	6	US-10-450-763-40822	Sequence 40822, A
107	109	5.2	646	6	US-10-852-335A-143	Sequence 143, App
108	108.5	5.2	1115	6	US-10-184-644-440	Sequence 440, Appl
109	108.5	5.2	1115	6	US-11-025-607-58	Sequence 58, Appl
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111	108	5.2	628	7	US-11-043-591-103	Sequence 103, App
112	107.5	5.1	241	7	US-10-499-710-2	Sequence 2, Appl
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114	107	5.1	332	5	US-10-038-956-5	Sequence 5, Appli
115	107	5.1	732	7	US-11-054-515-1648	Sequence 1648, Ap
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117	106.5	5.1	249	7	US-11-054-515-1986	Sequence 1986, A
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121	106.5	5.1	822	6	US-10-287-436A-1201	Sequence 1201, Ap
122	106.5	5.1	822	6	US-10-287-436A-1202	Sequence 1202, Ap
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142	104	5.0	1235	7	US-11-043-591-34	Sequence 34, App1
143	104	5.0	1176	7	US-11-043-591-35	Sequence 35, App1
144	104	5.0	1267	7	PCT-US05-02351-115	Sequence 115, App
145	104	5.0	1356	7	US-11-021-951-1115	Sequence 1115, App
146	104	5.0	1356	7	US-11-043-770-555	Sequence 555, App
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155	103.5	4.9	862	7	US-11-033-545-427	Sequence 427, App
156	103.5	4.9	1030	8	US-60-651-509-637	Sequence 637, App
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158	103	4.9	771	7	US-11-054-515-1646	Sequence 1646, Ap
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164	102	4.9	702	1	US-10-794-514A-301	Sequence 301, App
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213	96.5	4.6	1573	7	PCT-US03-41242-63	Sequence 63, Appl
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227	95	4.5	1904	6	PCT-US04-23166A-1729	Sequence 1729, Ap
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229	94.5	4.5	1863	7	PCT-US04-23166A-731	Sequence 731, App
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256	93	4.4	319	7	US-11-032-773-955	Sequence 955, Appl
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260	92.5	4.4	245	1	PCT-US04-42360-295	Sequence 295, App
261	92.5	4.4	248	7	US-11-054-515-848	Sequence 848, App
262	92.5	4.4	248	7	US-11-054-515-953	Sequence 953, App
263	92.5	4.4	250	7	US-11-054-515-2074	Sequence 2074, Ap
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265	92.5	4.4	282	6	US-11-050-926-348	Sequence 348, App
266	92.5	4.4	360	6	US-10-450-763-54272	Sequence 54272, A
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270	92.5	4.4	764	8	US-60-651-509-465	Sequence 465, App
271	92.5	4.4	764	8	US-60-651-509-466	Sequence 466, App
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281	92	4.4	552	7	US-11-028-058-9	Sequence 9, Appli
282	92	4.4	583	7	US-11-051-454-12	Sequence 12, Appl
283	92	4.4	583	8	US-60-651-509-418	Sequence 418, App
284	92	4.4	583	8	US-11-054-515-1212	Sequence 1212, Ap
285	91.5	4.4	251	7	US-11-054-515-1229	Sequence 1229, Ap
286	91.5	4.4	252	7	US-11-054-515-1713	Sequence 1713, Ap
287	91.5	4.4	433	1	US-11-021-951-129	Sequence 129, Appl
288	91.5	4.4	647	1	PCT-US04-31825-96	Sequence 96, Appl
289	91.5	4.4	726	8	US-60-651-509-634	Sequence 634, App
290	91.5	4.4	1048	6	US-10-520-783-22	Sequence 22, Appli
291	91	4.4	240	7	US-11-054-515-1391	Sequence 1391, Ap
292	91	4.4	250	7	US-11-054-515-1867	Sequence 1867, Ap
293	91	4.4	398	8	US-60-651-509-522	Sequence 522, App
294	91	4.3	398	8	US-60-651-509-527	Sequence 527, App
295	91	4.3	438	6	US-10-450-763-45185	Sequence 45185, A
296	90.5	4.3	200	8	US-60-651-509-99	Sequence 99, Appl
297	90.5	4.3	224	7	US-11-043-591-111	Sequence 111, Appl
298	90.5	4.3	244	7	US-11-054-515-1491	Sequence 1491, Ap
299	90.5	4.3	244	7	US-11-054-515-1507	Sequence 1507, Ap
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301	90.5	4.3	248	7	US-11-054-515-2091	Sequence 2091, Ap
302	90.5	4.3	250	7	US-11-054-515-859	Sequence 859, App
303	90.5	4.3	250	7	US-11-054-515-1383	Sequence 1383, Ap
304	90.5	4.3	251	7	US-11-054-515-1479	Sequence 1479, Ap
305	90.5	4.3	251	7	US-11-054-515-1774	Sequence 1774, Ap
306	90.5	4.3	251	7	US-11-054-515-1800	Sequence 1800, Ap
307	90.5	4.3	260	7	US-11-054-515-1244	Sequence 1244, Ap
308	90.5	4.3	473	8	US-60-651-509-378	Sequence 378, App
309	90.5	4.3	479	1	PCT-US04-43806-33	Sequence 33, Appl
310	90.5	4.3	479	1	US-11-024-251-33	Sequence 33, Appl
311	90.5	4.3	733	6	US-10-450-763-58502	Sequence 58502, A
312	90.5	4.3	784	6	US-11-026-545-45	Sequence 45, Appl
313	90	4.3	245	7	US-11-054-515-1547	Sequence 1547, Ap
314	90	4.3	246	7	US-11-054-515-1192	Sequence 1192, Ap
315	90	4.3	251	7	US-11-054-515-852	Sequence 852, App
316	90	4.3	251	7	US-11-054-515-1074	Sequence 1074, Ap
317	90	4.3	252	7	US-11-054-515-1145	Sequence 1145, Ap
318	90	4.3	252	7	US-11-054-515-1590	Sequence 1590, Appl
319	90	4.3	375	7	PCT-US04-38197-59	Sequence 59, Appl
320	90	4.3	1019	7	US-11-033-545-454	Sequence 454, App
321	89.5	4.3	178	6	US-10-450-763-36692	Sequence 36692, A
322	89.5	4.3	245	7	US-11-054-515-1528	Sequence 1528, Ap
323	89.5	4.3	245	7	US-11-054-515-845	Sequence 845, App
324	89.5	4.3	251	7	US-11-054-515-853	Sequence 853, App
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326	89.5	4.3	251	7	US-11-054-515-961	Sequence 961, App
327	89.5	4.3	251	7	US-11-054-515-962	Sequence 962, App
328	89.5	4.3	251	7	US-11-054-515-1073	Sequence 1073, Ap
329	89.5	4.3	251	7	US-11-050-926-332	Sequence 332, App
330	89.5	4.3	251	7	US-11-054-515-1107	Sequence 1107, Ap
331	89.5	4.3	251	7	US-11-054-515-1808	Sequence 1808, Ap
332	89.5	4.3	252	7	US-11-054-515-1811	Sequence 1811, Ap
333	89.5	4.3	252	7	US-11-054-515-1129	Sequence 1129, Ap
334	89.5	4.3	252	7	US-11-054-515-1103	Sequence 1103, Ap
335	89	4.3	282	8	US-60-651-509-525	Sequence 525, App
336	89	4.3	312	6	US-10-450-763-46426	Sequence 46426, A
337	89	4.3	468	6	US-10-450-763-58501	Sequence 58501, A
338	89	4.3	248	6	US-11-050-926-219	Sequence 219, App
339	89	4.3	248	6	US-10-938-061-136	Sequence 136, App
340	89	4.3	879	6	US-10-936-626-136	Sequence 136, App
341	89	4.3	879	6	US-10-051-724-90	Sequence 90, Appl
342	89	4.3	749	6	US-10-450-763-48872	Sequence 48872, A
343	89	4.3	312	6	US-10-450-763-46426	Sequence 46426, A
344	89	4.3	282	8	US-60-651-509-524	Sequence 524, App
345	89	4.3	282	8	US-60-651-509-523	Sequence 523, App
346	89	4.3	260	6	US-10-450-763-50295	Sequence 50295, A
347	89	4.3	253	7	US-11-054-515-1974	Sequence 1974, Ap
348	89	4.2	248	6	US-11-050-926-219	Sequence 219, App
349	89	4.2	248	6	US-10-938-061-136	Sequence 136, App
350	88.5	4.2	140	6	US-10-450-763-52697	Sequence 52697, A
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353	88.5	4.2	247	7	US-11-054-515-1764	Sequence 1764, Ap
354	88.5	4.2	247	7	US-11-054-515-2072	Sequence 2072, Ap
355	88.5	4.2	247	7	US-11-054-515-1388	Sequence 1388, Ap
356	88.5	4.2	248	7	US-11-054-515-1529	Sequence 1529, Ap
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360	88.5	4.2	251	7	US-11-054-515-1297	Sequence 1297, Ap
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362	88.5	4.2	256	7	US-11-054-515-1297	Sequence 1297, Ap
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364	88.5	4.2	257	6	PCT-US04-38197-36	Sequence 36, Appl
365	88.5	4.2	592	6	US-11-030-653-12	Sequence 12, Appl
366	88.5	4.2	824	6	US-11-030-653-14	Sequence 14, Appl
367	88.5	4.2	1215	8	US-11-033-545-321	Sequence 321, App
368	88.5	4.2	1235	8	US-10-450-763-35137	Sequence 35137, A
369	88	4.2	179	8	US-60-651-509-270	Sequence 270, App
370	88	4.2	179	8	US-60-651-509-271	Sequence 271, App
371	88	4.2	247	7	US-11-054-515-927	Sequence 927, App
372	88	4.2	247	7	US-11-054-515-948	Sequence 948, App
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374	88	4.2	249	7	US-11-054-515-819	Sequence 819, App
375	88	4.2	252	7	US-11-054-515-1128	Sequence 1128, Ap
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377	88	4.2	257	7	US-11-054-515-1240	Sequence 1240, Ap
378	88	4.2	293	7	US-11-054-515-709	Sequence 709, App
379	88	4.2	542	6	PCT-US04-23166A-709	Sequence 709, App
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381	88	4.2	787	5	US-09-880-573B-110	Sequence 110, App
382	87.5	4.2	205	5	US-11-033-545-362	Sequence 362, App
383	87.5	4.2	205	7	US-11-033-545-505	Sequence 505, App
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387	87.5	4.2	244	7	US-11-054-515-1569	Sequence 1569, Ap
388	87.5	4.2	248	7	US-11-054-515-1363	Sequence 1363, Ap
389	87.5	4.2	251	7	US-11-054-515-884	Sequence 884, App
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393	87.5	4.2	1907	6	US-10-712-892A-34	Sequence 34, Appl
394	87	4.1	244	7	US-11-054-515-1845	Sequence 1845, Ap
395	87	4.1	247	7	US-11-054-515-1328	Sequence 1328, App
396	87	4.1	248	1	PCT-US04-38197-275	Sequence 275, App
397	87	4.1	248	7	US-11-054-515-835	Sequence 835, App
398	87	4.1	249	7	US-11-054-515-472	Sequence 472, App
399	87	4.1	250	7	US-11-054-515-1851	Sequence 1851, Ap
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403	87	4.1	412	6	US-10-013-173A-6	Sequence 6, Appli
404	87	4.1	548	7	US-11-028-058-11	Sequence 11, Appli
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406	87	4.1	640	7	US-11-028-058-5	Sequence 5, Appli
407	87	4.1	653	1	PCT-US04-42360-74	Sequence 74, Appl
408	87	4.1	653	7	US-11-058-709-10	Sequence 10, Appl
409	87	4.1	924	7	US-10-947-476-6	Sequence 6, Appli
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411	86.5	4.1	237	7	US-11-054-515-1941	Sequence 1941, Ap
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414	86.5	4.1	251	7	US-11-054-515-882	Sequence 882, App
415	86.5	4.1	251	7	US-11-054-515-887	Sequence 887, App
416	86.5	4.1	251	7	US-11-054-515-968	Sequence 968, App
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431	86.5	4.1	568	8	US-60-643-717-3396	Sequence 3396, Ap
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435	86	4.1	243	7	US-11-054-515-1863	Sequence 1863, Ap
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443	86	4.1	255	1	PCT-US04-38197-1227	Sequence 1227, App
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445	86	4.1	262	1	PCT-US04-38197-278	Sequence 278, App
446	86	4.1	590	7	US-11-058-709-12	Sequence 12, Appl
447	86	4.1	656	7	US-11-030-653-38	Sequence 38, Appl
448	86	4.1	713	7	US-11-030-653-26	Sequence 26, Appl
449	85.5	4.1	1336	6	US-10-712-892A-33	Sequence 33, Appl
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451	85.5	4.1	237	6	US-10-450-763-2006	Sequence 2006, Ap
452	85.5	4.1	237	7	US-11-054-515-2036	Sequence 2036, Ap
453	85.5	4.1	243	7	US-11-054-515-2056	Sequence 2056, Ap
454	85.5	4.1	248	7	US-11-054-515-1890	Sequence 1890, Ap
455	85.5	4.1	250	7	US-11-054-515-1723	Sequence 1723, Ap
456	85.5	4.1	251	7	US-11-054-515-875	Sequence 875, App
457	85.5	4.1	251	7	US-11-054-515-879	Sequence 879, App
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494	85.5	4.1	479	6	US-10-450-763-51419	Sequence 51419, A
495	85.5	4.1	1375	6	US-10-450-763-32231	Sequence 32231, A
496	85	4.1	1495	6	US-10-450-763-34736	Sequence 34736, A
497	85	4.1	234	8	US-60-651-509-269	Sequence 269, App
498	85	4.1	240	7	US-11-054-515-1711	Sequence 1711, Ap
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500	85	4.1	249	7	US-11-054-515-2113	Sequence 2113, Ap
501	85	4.1	249	7	US-11-054-515-499	Sequence 499, App
502	85	4.1	252	7	US-11-054-515-737	Sequence 737, App
503	85	4.1	252	6	US-10-882-333A-184	Sequence 184, App
504	85	4.1	254	6	US-10-450-763-43249	Sequence 43249, A
505	85	4.1	258	8	US-60-651-509-416	Sequence 416, App
506	85	4.1	258	8	US-60-651-509-415	Sequence 415, App
507	85	4.1	295	8	US-60-651-509-417	Sequence 417, App
508	85	4.1	479	7	US-11-032-232-8	Sequence 8, Appli
509	85	4.1	479	6	US-10-450-763-48879	Sequence 48879, A
510	85	4.1	512	6	US-10-040-706-5	Sequence 5, Appli
511	85	4.1	532	6	US-10-450-763-444-2817	Sequence 2817, Ap
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514	85	4.1	651	7	US-11-054-515-1787	Sequence 1787, Ap
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518	84.5	4.0	244	7	US-11-054-515-1582	Sequence 1582, Ap
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527	84.5	4.0	251	7	US-11-054-515-1824	Sequence 1824, Ap
528	84.5	4.0	251	7	US-11-054-515-1833	Sequence 1833, Ap
529	84.5	4.0	259	1	PCT-US04-38197-161	Sequence 161, App
530	84.5	4.0	262	1	PCT-US04-38197-162	Sequence 162, App
531	84.5	4.0	266	1	PCT-US04-38197-163	Sequence 163, App
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534	84.5	4.0	568	6	US-10-450-763-48871	Sequence 8, Appli
535	84.0	4.0	568	8	US-60-643-717-7228	Sequence 7228, Ap
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542	84	4.0	240	7	US-11-054-515-2105	Sequence 2105, Ap
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826	79.5	3.8	259	8	US-60-643-717-3367	Sequence 3367, Ap
827	79.5	3.8	568	8	US-60-643-717-3031	Sequence 3031, Ap
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834	79.5	3.8	1663	1	PCT-US04-42360-424	Sequence 424,	App
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839	79	3.8	242	7	US-11-054-515-2046	Sequence 2046,	Ap
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1348	75	3.6	761	9	US-11-035-599-29	Sequence 29, Appl
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1359	75	3.6	2316	6	US-10-287-434A-566	Sequence 566, A
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1364	74.5	3.6	218	6	PCT-US04-937-596-33	Sequence 33, Appl
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1367	74.5	3.6	240	7	US-10-450-515-1912	Sequence 1912, Ap
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1395	74.5	3.6	250	7	US-11-054-515-1484	Sequence 1484, Ap
1396	74.5	3.6	251	7	US-11-054-515-2066	Sequence 2066, Ap
1397	74.5	3.6	251	7	US-11-054-515-1594	Sequence 1594, Ap
1398	74.5	3.6	252	7	US-11-054-515-976	Sequence 976, App
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1401	74.5	3.6	255	7	US-11-054-515-1065	Sequence 1065, Ap
1402	74.5	3.6	255	7	US-11-054-515-1261	Sequence 1261, Ap
1403	74.5	3.6	250	8	US-60-643-717-9005	Sequence 9005, Ap
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1406	74.5	3.6	568	8	US-60-643-717-13771	Sequence 13771, A
1407	74.5	3.6	568	8	US-60-643-717-10729	Sequence 10729, A
1408	74.5	3.6	568	8	US-60-643-717-36702	Sequence 36702, A
1409	74.5	3.6	972	6	US-10-450-763-36724	Sequence 36724, A
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1472	74	3.5	252	7	US-11-054-515-1518	Sequence 1518, Ap
1473	74	3.5	252	7	US-11-054-515-1992	Sequence 1992, Ap
1474	74	3.5	253	7	US-11-054-515-1502	Sequence 1502, Ap
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1482	74	3.5	365	7	US-11-027-878-4389	Sequence 4389, Ap
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1484	74	3.5	365	7	US-11-028-204-4389	Sequence 4389, Ap
1485	74	3.5	365	7	US-11-027-877-4389	Sequence 4389, Ap
1486	74	3.5	365	7	US-11-027-879-4389	Sequence 4389, Ap
1487	74	3.5	365	7	US-11-028-149-4389	Sequence 4389, Ap
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1500	74	3.5	375	1	PCT-US04-17965-1029	Sequence 1029, Ap

ALIGNMENTS

RESULT 1
US-09-978-191C-52
Sequence 52, Application US/09978191C
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191C
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649

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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 623
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; SEQ ID NO 52
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-191C-52

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Matches   321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
US-10-986-822-6
; Sequence 6, Application US/10986822
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: YUE, Henry
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: GORGONE, Gina A.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: PROTEIN TRANSPORT-ASSOCIATED MOLECULES
; FILE REFERENCE: PF-0577 PCT
; CURRENT APPLICATION NUMBER: US/10/986,822
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US/09/763,902
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: 60/098,206
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
;
; SEQ ID NO 6
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No.18712175CD1
US-10-986-822-6
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Db    147 TEAPTTMTYPLKATSTVKQSWDWTTDMDG 175


RESULT 3
US-10-523-834-330
; Sequence 330, Application US/10523834
; GENERAL INFORMATION:
; APPLICANT: diaDexus, Inc.
; APPLICANT: Macina, Roberto
; APPLICANT: Salceda, Susana
; APPLICANT: Liu, Chenghua
; APPLICANT: Sun, Yongming
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and P
; FILE REFERENCE: DEX-0443
; CURRENT APPLICATION NUMBER: US/10/523,834
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/401,469
; PRIOR FILING DATE: 2002-08-06
; SOFTWARE: Patentin version 3.1
; NUMBER OF SEQ ID NOS: 396
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; SEQ ID NO 330
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-523-834-330
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Matches   65;  Conservative  36;  Mismatches  93;  Indels  51;  Gaps  11;

Qy      1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
          ||| |||   ||  :  ||||||||  :  | :|:|
Db     17 LAILLCSLALGSVTVHS-SEPEVRIPEN-----NPVKLSCAY---SGFSSRPVEW----  62

Qy     61 GSDPVTIFLRDSSGDHIQQAAKYQGRLHVSHK-----VPGDVSLQLSTLEMDRSHYTCEV 115
          :||||||||||||||:||  : :  : : |||    |  :  : : ||  :  :|||||
Db     63 ------KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITPFKSVTRB--DTGTYTCMV 111

Qy    116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGPTVPQGMRISLQCQAR-GSPPIS 174
          : : |   : | ||||||||||||||||||||||||||:  : : |||||||  |||||:
Db    112 SEEGGNSYGEVKVKLIVL----VPPSKPTVNIPS---SATIGNRAVLTCSEQDGSPSE 163

Qy    175 YIWYK-----QQTN------NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH 222
          ||  |     | |        :| : |:  :  ::| |: : || :|
Db    164 YTWFKDGIVMPINPKSTRAFSNSSYVLNPTGELVFDPLSASDTGEYSCEARNGYGTPMT 223

Qy    223 SDIVK 227
          |:|:|
Db    224 SNAVR 228
```

RESULT 4
US-10-155-282B-11
; Sequence 11, Application US/10155282B
; GENERAL INFORMATION:
; APPLICANT: Brookhaven Science Associates
; APPLICANT: Freimuth, Paul I
; TITLE OF INVENTION: Recombinant Soluble Adenovirus Receptor
; FILE REFERENCE: BSA 02-14
; CURRENT APPLICATION NUMBER: US/10/155,282B
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/236,423
; PRIOR FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 11
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-155-282B-11

Query Match   7.6%;   Score 159; DB 6; Length 365;
Best Local Similarity 23.2%; Pred. No. 7.3e-06;
Matches   81; Conservative 49; Mismatches 119; Indels 100; Gaps 20;

```
Qy   1 MGILLGLLLLGHLTVDTYGRPI-LEVPESVTGPWKGD-VNLPCTY------DPLQGYTQ  51
         ::||| |||||:| ||||| |:|  : |:  ||| |||  ||||:            ||
Db   1 MALLLCFVLL--CGVVDFARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDQGPLD----  54

Qy  52 VLVKWLVQRGS---DPVTIFLRDSSGDHIQQAKY---QGRLHVSHK--VPGDVSLQLST 102
         :|: |         |||:  :  : || |||  : |    ||||||    |||:||||:
Db  55 --IEWLISPADNQKVDQVIILY---SGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTN 109

Qy 103 LEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPT----VTTGSGYGFTVPQG 158
         |  |  |::| |:|  | |        || ||  |  |:|| |        ||  ||| |
Db 110 LQLSDIGTYQCKVK-KAPG--------VANKKIHLVLVLVKPSGARCYVDGS----EEIG 155

Qy 159 MRISLQCQAR-GSPPISYIWYKQQTNNQEP---IKVATLSTLLFKPAVIADSGSYFCTAK 214
         | |:|:|   |||| ::  |:| :  || |    |||| |:||||:||||||||| |  |
Db 156 SDFKIKCEPKEGSLPLQYEWQKLSDSQKMPTSWLAEMTSSVISVKNASSEYSGTYSCTVR 215

Qy 215 GQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGET 274
         |:|||:|   |:|:  |              ||:|:|           |           
Db 216 NRVGSDQ---------------CLLRLNVVPPSN----KA------------GLIAGA 242

Qy 275 SAGPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKTSQOEHVYEAARAH 323
         :||||||||||:||:|| ||||||||||||:::   |        ||
Db 243 IIG---TLLALALIGLIIFCC------------RKKRREEKYEKEVHH 275
```

RESULT 5
US-60-651-509-101
Sequence 101, Application US/6065l509
; GENERAL INFORMATION:
; APPLICANT: RUBEN, Steven et al.
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001578
; CURRENT APPLICATION NUMBER: US/60/651,509
; CURRENT FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 1940
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-651-509-101

Query Match   7.6%;   Score 159; DB 8; Length 365;
Best Local Similarity 23.2%; Pred. No. 7.3e-06;
Matches   81; Conservative 49; Mismatches 119; Indels 100; Gaps 20;

```
Qy   1 MGILLGLLLLGHLTVDTYGRPI-LEVPESVTGPWKGD-VNLPCTY------DPLQGYTQ  51
         ::||| |||||:| ||||| |:|  : |:  ||| |||  ||||:            ||
Db   1 MALLLCFVLL--CGVVDFARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDQGPLD----  54
```

RESULT 6
US-60-651-509-103
Sequence 103, Application US/60651509
; GENERAL INFORMATION:
; APPLICANT: RUBEN, Steven et al.
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001578
; CURRENT APPLICATION NUMBER: US/60/651,509
; CURRENT FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 1940
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-651-509-103

Query Match   7.6%;   Score 159; DB 8; Length 365;
Best Local Similarity 23.2%; Pred. No. 7.3e-06;
Matches   81; Conservative 49; Mismatches 119; Indels 100; Gaps 20;

```
Qy   1 MGILLGLLLLGHLTVDTYGRPI-LEVPESVTGPWKGD-VNLPCTY------DPLQGYTQ  51
         ::||| |||||:| ||||| |:|  : |:  ||| |||  ||||:            ||
Db   1 MALLLCFVLL--CGVVDFARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDQGPLD----  54

Qy  52 VLVKWLVQRGS---DPVTIFLRDSSGDHIQQAKY---QGRLHVSHK--VPGDVSLQLST 102
         :|: |         |||:  :  : || |||  : |    ||||||    |||:||||:
Db  55 --IEWLISPADNQKVDQVIILY---SGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTN 109

Qy 103 LEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPT----VTTGSGYGFTVPQG 158
         |  |  |::| |:|  | |        || ||  |  |:|| |        ||  ||| |
Db 110 LQLSDIGTYQCKVK-KAPG--------VANKKIHLVLVLVKPSGARCYVDGS----EEIG 155

Qy 159 MRISLQCQAR-GSPPISYIWYKQQTNNQEP---IKVATLSTLLFKPAVIADSGSYFCTAK 214
         | |:|:|   |||| ::  |:| :  || |    |||| |:||||:||||||||| |  |
Db 156 SDFKIKCEPKEGSLPLQYEWQKLSDSQKMPTSWLAEMTSSVISVKNASSEYSGTYSCTVR 215

Qy 215 GQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGET 274
         |:|||:|   |:|:  |              ||:|:|           |           
Db 216 NRVGSDQ---------------CLLRLNVVPPSN----KA------------GLIAGA 242

Qy 275 SAGPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKTSQOEHVYEAARAH 323
         :||||||||||:||:|| ||||||||||||:::   |        ||
Db 243 IIG---TLLALALIGLIIFCC------------RKKRREEKYEKEVHH 275
```

RESULT 7
US-09-978-191C-59
; Sequence 59, Application US/09978191C
; GENERAL INFORMATION:

```
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191C
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 623
; SEQ ID NO 59
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-978-191C-59

Query Match             7.6%;  Score 158.5;  DB 5;  Length 373;
Best Local Similarity   22.2%;  Pred. No. 8.3e-06;
Matches   91;  Conservative   64;  Mismatches 154;  Indels 101;  Gaps   20;

Qy         1 MGILLGLILLGHL--TVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLV 58
             |||::||:|||::|    ::|::: |:|||::| ||:|||||:| :|:: || :|:::|
Db         1 MSLILLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLP--EKDTLD-----IEWLL 53

Qy        59 --QRGSDPVTIFLRDSSGDHIQQ----AKYQGRL-HVSHKVPGDVSLQLSTLEMDDRSHYT 112
               :|:|| :| :| :: |:  |    | : |||  |:  | || :: |||::::|:| |
Db        54 TDNEGNQKVVI---TYSSRHVNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYT 110

Qy       113 CEVTWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQ-ARGSP 171
             | |||||||:||:|| || :|||||:|||||||||||||||| |||:|||||||  ||||
Db       111 CKV----KNSGRYWSHVILKVLVRP----SKPKCELEG----ELTEGGSDLITLQCESSSGTE 160

Qy       172 PISYIWYKQQTNNQEPIKVATLSTL-----LFKPAVIADSGSYFCTAKGQVGSEQHS 223
             | :|||||:||:||||:|||:||     |||||||||||||||||| ||||:||
Db       161 PIVYYWQRIREKEGEDERLPPKSRIDYNHPGRVLLQNLTMSYSGLYQCTAGNEAGKE--S 218

Qy       224 DIVKFVVKDSSKLLKTKTEAPTTMTYPLKATSTVKQSMWDWTTDMDGYLGETSAGPGKSLP 283
             ||:| ::||:::||||||||||:|| ||:|||:||||: |||||||||||:|||| |||
Db       219 CVVRVTVQ----------- 240

Qy       284 VFAIILIISLCCMVVFTMAYIMLCRKTSQQ---------EHVYEAARA-HAREANDSGETMR 335
             ||||||||::|||||||||||||||||||         |||| |||| |:|:|:|:|:|:|
Db       241 IVAGALII------FLLVWLLIRRKDKERYEEEERPNEIREDEAPKARLVKPSSSSSG 293

Qy       336 VAIFASGCGSSDEPTS--------QNLGNNYSDEPCCIG-QEYQOIIA-QINGN 376
             | || ||| ::|||          ||| :|||:| ||  |:|||: |:||
Db       294 SRSSRSGSGSSSTRSTANSASRSQRTLSTDAAPQFGIATQAYSLVGPEVRGS 343
```

```
US-10-523-834-331
; Sequence 331, Application US/10523834
; GENERAL INFORMATION:
; APPLICANT: diaDexus, Inc.
; APPLICANT: Macina, Roberto
; APPLICANT: Salceda, Susana
; APPLICANT: Liu, Chenghua
; APPLICANT: Sun, Yongming
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Ovarian Specific Genes and P
; FILE REFERENCE: DEX-0443
; CURRENT APPLICATION NUMBER: US/10/523,834
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/401,469
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 396
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 331
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-523-834-331

Query Match             7.5%;  Score 157.5;  DB 6;  Length 351;
Best Local Similarity   23.0%;  Pred. No. 9.4e-06;
Matches   67;  Conservative   38;  Mismatches  95;  Indels  91;  Gaps  12;

Qy         1 MGILLGLILLGHLITVDTYGRPILEVPES---VTGPWKG--- 35
             ||||| || || |:||:||| || ||::    ||||:|
Db        17 LAILLCSLALGSVTVHS-SEPEVRIPENNRELGGAMEGVRVSSCRPPGDLESTQPSLQFG 75

Qy        36 --------------DVNLPCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSG 74
                           ||:||||||||||||||:||:|  ||||||:|||||
Db        76 AVPHLVYLLLFFLRLILTLSAAVKLSCAY---SGFSSPRVEW-------KFDQ 119

Qy        75 DHIQQAKYQGRLHVSHK------VPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDK 129
             ::| |||:|||:||::        |||||||||||||||||||||:|||||||:||:||
Db       120 DTTRLVCYNNKITASYEDRVTFLPTGITFKSVTRE--DTGTYTCMVSEEGGNSYGEVKVK 177

Qy       130 ITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQAR-GSPPISYIWYK----QQTN- 183
             |||||||||:|||||||||| ||||:|||||||||:|| :| ||| ||| |     ||||
Db       178 LIVL---VPPSKPTVNIPS---SATIGNRAVLTCSEQDGSPPSEYIWFKDGIVMPINP 229

Qy       184 ------NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVK 227
                   ||:|||||| || ::|||||||||||||||||: ||||||:||
Db       230 KSTRAFSNSSYVLNPTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVR 280
```

```
US-10-450-763-32378
; Sequence 32378, Application US/10450763
; GENERAL INFORMATION:
```

; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 32378
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (564)..(597)
; OTHER INFORMATION: RECEPTOR INTERLEUKIN-1 PRECURSOR domain identified by
; OTHER INFORMATION: eMATRIX, accession number PD028708, p-value=7.400e-10, raw score
; OTHER INFORMATION: 18.83
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (354)..(728)
; OTHER INFORMATION: Immunoglobulin domain identified by PFam, accession name ig,
; OTHER INFORMATION: E-value=1.4e-36, PFam score of 122.9
US-10-450-763-32378

Query Match   7.4%;   Score 156; DB 6;   Length 737;
Best Local Similarity 24.3%;   Pred. No. 3.2e-05;
Matches 73; Conservative 38; Mismatches 128; Indels 62; Gaps 14;

Qy   4 LIGLLLL-------------------------------GHLTVDTYGRPI-LEVPESVTGPWKGDVNL 39
              ||||||| | ::||| || |||| |: |
Db   465 LIGLLKIQETQDLDAGDYTCVAINEAGRATGKITLDVGSPPVFIQEPADVSMEIGSNVTL 524

Qy   40 PCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQ 99
              || | :: ||| | |: | | |: | | || :| |||
Db   525 PCY---VQGYPEPTIKW--RRLDNMPIFSRPFSVSSISQLR-TGALFILN------ 568

Qy   100 LSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGM 159
              | | |: ||| | |: || | :| ||:| ||
Db   569 --LWASDKGTYICEAENQFGKIQSETTVTVTGLVAPLIGIS-PSVA------ 617

Qy   160 RISLQCQ-ARGSPPISYIWYKQQTN-NQEP-IKVATLSTLLFKPAVIADSGSYFCTAKGQ 216
              | :| | || ||| | ||| : | :|| | :| | | || |
Db   618 QLTLPCTLLAGNPIPERRWIKNSAMLLQNPYITVRSDGSLHIERVQLQDGGEYTCVASNV 677

Qy   217 VGSEQHSDIVKF----VVKDSSKLLKTKTEAPTTMTYPLKATSTVKQS--WDWTTDMDGY 270
              | |:| :|:|: | :|| || | :| ||| :|| | | |||||
Db   678 AGTNNKITSVVVHVLPTIQHGQQILSTIEGIPVTL--PCKASGNPKPSVIWSKVNDTSSY 735

Qy   271 L 271
              :
Db   736 I 736

RESULT 10
PCT-US05-03880-128
; Sequence 128, Application PC/TUS0503880
; GENERAL INFORMATION:
; APPLICANT: INANA, GEORGE
; APPLICANT: McLAREN, MARGARET
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING RETINAL
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 39532-192229
; CURRENT APPLICATION NUMBER: PCT/US05/03880
; CURRENT FILING DATE: 2005-02-09
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 128

; LENGTH: 5622
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-03880-128

Query Match   7.4%;   Score 154.5; DB 1;   Length 5622;
Best Local Similarity 23.8%;   Pred. No. 0.00054;
Matches 93; Conservative 43; Mismatches 152; Indels 103; Gaps 20;

Qy   4 LIGLLLL-------------------------------GHLTVDTYGRPI-LEVPESVTGPWKGDVNL 39
              ||||||| | ::||| || |||| |: |
Db   753 LIGLLKIQETQDLDAGDYTCVAINEAGRATGKITLDVGSPPVFIQEPADVSMEIGSNVTL 812

Qy   40 PCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQ 99
              || | :: ||| | |: | | |: | | || :| |||
Db   813 PCY---VQGYPEPTIKW--RRLDNMPIFSRPFSVSSISQLR-TGALFILN------ 856

Qy   100 LSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGM 159
              | | |: ||| | |: || | :| ||:| ||
Db   857 --LWASDKGTYICEAENQFGKIQSETTVTVTGLVAPLIGIS-PSVA------ 905

Qy   160 RISLQCQ-ARGSPPISYIWYKQQTN-NQEP-IKVATLSTLLFKPAVIADSGSYFCTAKGQ 216
              | :| | || ||| | ||| : | :|| | :| | | || |
Db   906 QLTLPCTLLAGNPIPERRWIKNSAMLLQNPYITVRSDGSLHIERVQLQDGGEYTCVASNV 965

Qy   217 VGSEQHSDIVKF----VVKDSSKLLKTKTEAPTTMTYPLKATSTVKQS--WDWTTDMDGY 270
              | |:| :|:|: | :|| || | :| ||| :|| | | |||||
Db   966 AGTNNKITSVVVHVLPTIQHGQQILSTIEGIPVTL--PCKASGNPKPSVIWS--KKGELI 1021

Qy   273 ET------SAGPGKSLPVFAIILIS-------------LCCMVFTMAYIMLCRKTSQQEHVYEA 319
              :   :   : |: | |
Db   1022 STSSAKFSAGDADGSL---YVVSPGGEESGEVVCTATNTAGY----AKRKVQLTVY-- 1069

Qy   320 ARAHAREANDSGETMRVAIFAS--GCSDEP 348
                               | | | | |
Db   1070 ----------------VRPRVEGDQRGLSQDKP 1086

RESULT 11
US-11-049-637-2
; Sequence 2, Application US/11049637
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Donoho, Gregory
; TITLE OF INVENTION: Novel Human Hemicentin Proteins and Polynucleotides
; FILE REFERENCE: LEX-0235-USA
; CURRENT APPLICATION NUMBER: US/11/049,637
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US/09/953,096
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US 60/232,793
; PRIOR FILING DATE: 2000 09-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5518
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(5518)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-049-637-2

Query Match   7.3%;   Score 153.5; DB 7;   Length 5518;
Best Local Similarity 25.2%;   Pred. No. 0.00064;
Matches 80; Conservative 38; Mismatches 132; Indels 67; Gaps 15;

Qy   4 LIGLLLL-------------------------------GHLTVDTYGRPI-LEVPESVTGPWKGDVNL 39
              ||||||| | ::||| || |||| |: |
Db   753 LIGLLKIQETQDLDAGDYTCVAINEAGRATGKITLDVGSPPVFIQEPADVSMEIGSNVTL 812

RESULT 12
US-10-450-763-32476
; Sequence 32476, Application US/10450763
; GENERAL INFORMATION:
;   APPLICANT: Hyseq, Inc
;   TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;   FILE REFERENCE: 790CIP3/US
;   CURRENT APPLICATION NUMBER: US/10/450,763
;   CURRENT FILING DATE: 2003-06-11
;   PRIOR APPLICATION NUMBER: PCT/US01/08631
;   PRIOR FILING DATE: 2001-03-30
;   PRIOR APPLICATION NUMBER: 09/540,217
;   PRIOR FILING DATE: 2000-03-31
;   PRIOR APPLICATION NUMBER: 09/649,167
;   PRIOR FILING DATE: 2000-08-23
;   NUMBER OF SEQ ID NOS: 60736
;   SOFTWARE: Custom
; SEQ ID NO 32476
;   LENGTH: 434
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (270)..(303)
;   OTHER INFORMATION: RECEPTOR INTERLEUKIN-1 PRECURSOR domain identified by
;   OTHER INFORMATION: eMATRIX, accession number PD028708, p-value=7.400e-10, raw score
;   OTHER INFORMATION: 18.83
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (60)..(434)
;   OTHER INFORMATION: Immunoglobulin domain identified by Pfam, accession name ig,
;   OTHER INFORMATION: E-value=1.4e-36, Pfam score of 122.9
US-10-450-763-32476

Query Match   7.2%; Score 151; DB 6; Length 434;
Best Local Similarity   24.3%; Pred. No. 4.3e-05;
Matches   71; Conservative   38; Mismatches 123; Indels   60; Gaps   13;

Qy   4 LIGLLLL-------------------------GHLTVDTYGRPI-LEVPESVTGPWKGDVNL 39
              |||.|||.   :|::| |::|| .|..|:|..|.
Db   171 LIGLLLKIQETQDLDAGDYTCVAINEAGRATGKITLDVGSPPVFIQEPADVSMEIGSNVTL 230

Qy   40 PCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSGDHIQAKYQGRLHVSHKVPGDVSLQ 99
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   231 PCY--VQGYPEPTIKW--RRLDNMPIFSRPFSVSSISQLR-TGALFILN------- 274

Qy   100 LSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGM 159
              |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   231 PCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSGDHIQAKYQGRLHVSHKVPGDVSLQ 99

Qy   160 RISLQCQ-ARGSPPISYIWYKQQTN-NQEP-IKVATLSTLLFKPAVIADSGGSYFCTAKGQ 216
              ||||||| |.||||:|||||.||.| |.|| |..|:||||||:.||:|||.|||||:.|
Db   906 QLILPCTLLAGNPIPERRWIKNSAMLLQNPYITVRSDGSLHIERVQLQDGGEYTCVASNV 965

Qy   217 VGSEQHSDIVKF----VVRDSSKLLLKTKTEAPTTMTYPLKATSTVKQSWDWTTDMDGYIG 272
              ||||||||||| ||||||||||||||||||||||||||||||||||||
Db   966 AGTNNKTTSVVVHVLPTIQHGQQILSTIEGIPVTL--PCKASGNPKPSVIWS--KKGELI 1021

Qy   273 ET-----SAGPGKSLPV 284
              |: |:||.|:||
Db   1022 STSSAKFSAGADGSLYV 1038

RESULT 13
US-10-450-763-52760
; Sequence 52760, Application US/10450763
; GENERAL INFORMATION:
;   APPLICANT: Hyseq, Inc
;   TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;   FILE REFERENCE: 790CIP3/US
;   CURRENT APPLICATION NUMBER: US/10/450,763
;   CURRENT FILING DATE: 2003-06-11
;   PRIOR APPLICATION NUMBER: PCT/US01/08631
;   PRIOR FILING DATE: 2001-03-30
;   PRIOR APPLICATION NUMBER: 09/540,217
;   PRIOR FILING DATE: 2000-03-31
;   PRIOR APPLICATION NUMBER: 09/649,167
;   PRIOR FILING DATE: 2000-08-23
;   NUMBER OF SEQ ID NOS: 60736
;   SOFTWARE: Custom
; SEQ ID NO 52760
;   LENGTH: 361
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (56)..(232)
;   OTHER INFORMATION: Immunoglobulin domain identified by Pfam, accession name ig,
;   OTHER INFORMATION: E-value=9.6e-19, Pfam score of 65.4
US-10-450-763-52760

Query Match   7.0%; Score 146.5; DB 6; Length 361;
Best Local Similarity   24.5%; Pred. No. 8.3e-05;
Matches   60; Conservative   31; Mismatches   91; Indels   63; Gaps   11;

Qy   9 LIGHLTVDTYGR-PILEVPESVTGPWKGDVNLPC------TYPDPLQGYTQVLVKWLVQRG 61
              ||:||||||| | || .|.|..|.|||:||: || |||||||||||||||||
Db   37 LIGAVNLKSSNRIPVVQEFES----VELSCIITDSQTSDP----RIEWKKIQD 81

Qy   62 SDPVTIFLRDSSGDHIQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPD 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   82 EQTTYVFFDN------KIQGDLAGRAEILGKTLSLKIWNVTRRDSALIYRCEVVARND- 131

Qy   122 GNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQAR-GSPPISYIWYKQ 180
              |.|||||:||||:||.|:.|..|...:|.|||.|.|.|||||||| | ||||:|||||.|
Db   122 GNQVVRDKITELRVQKLSVSKPTVTTGSSGYGFTVPQGMRISLQCQAR-GSPPISYIWYKQ 180

Qy   181 QTNNQEPIKV-----------ATLSTLLFKPAVIADSGGSYFCTAKGQVGS----E 220
              |||.|.|..| |||||||||||.||||.||||||.|.| | |
Db   132 -----RKEIDEIAIEVTVQVKP-VTPVCRVPKAVPVGKMATLHCQGEXGPPPAHYSWYR- 184

Qy   221 QHSDI 225
              |..||
Db   185 --NDVPLPTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 241

Qy   221 QEMEV 246
              |..|.
Db   242 QEMEV 246

RESULT 14
US-10-852-335A-139
; Sequence 139, Application US/10852335A
; GENERAL INFORMATION:
;   APPLICANT: HIDI S. PHILLIPS
;   TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
;   TITLE OF INVENTION: Treatment of Tumors of Glial Origin
;   FILE REFERENCE: P5103R1-US

Qy   160 RISLQCQ-ARGSPPISYIWYKQQTN-NQEP-IKVATLSTLLFKPAVIADSGGSYFCTAKGQ 216

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; CURRENT APPLICATION NUMBER: US/10/852,335A
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 60/548,299
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/473,238
; PRIOR FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 190
; SEQ ID NO 139
; LENGTH: 3707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-852-335A-139

  Query Match            25.1%;  Pred. No. 0.006;  DB 6;  Length 3707;
  Best Local Similarity   6.6%;
  Matches   66;  Conservative  31;  Mismatches 105;  Indels  61;  Gaps  14;
  Score 139.5;

Qy    13 LTVDT-----YGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQRGSDPVTIF 68
         : ||      ||: :|| :   |     ::|    | ::
Db  2521 LIVDTGTVAPGTPQVVEES----------ELTLEA--GHTATL--HCSATGNPPPT-- 2563

Qy    69 LRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRD 128
         |   : :  |           |      |
Db  2564 ------------IHWSKLRAPLPWQHRIEGN-TLVIPRVAQQDSGQYICNAT----NSAGHT 2608

Qy   129 KITELRVQKLSVSKPTVTTGSGYGFTVPQ------GMRISLQCQQARGSPPISYIWYKQQT 182
         : |:  :                           |:|:|     |||:|:|::|||
Db  2609 EATVV-----LHVESPP-------YATIIPEHTSAQPGNLVQLQCLAHGTPPLTYQW--SLV 2656

Qy   183 NNQEPIKVATLSTLL-FKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKT 241
            ::      || |   ||||||||||| :||| ::|||
Db  2657 GGVLPEKAVVRNQLLREPTVPEDSGRYRCQVSNRVGSAE--AFAQVLVQGSSSNLPDTS 2714

Qy   242 ----EAPTTMTYPLKAITSTVKQS 260
             :   :|   :||:|
Db  2715 IPQGSTPTVQVTFQLETRNIGAS 2737
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RESULT 15
; Sequence 272, Application PC/TUS0502350
; GENERAL INFORMATION:
;  APPLICANT: Ayalon-Soffer, Michal
;  APPLICANT: Levine, Zurit
;  APPLICANT: Sella-Tavor, Osnat
;  APPLICANT: Diber, Alex
;  APPLICANT: Shemesh, Ronen
;  APPLICANT: Toporik, Amir
;  APPLICANT: Rotman, Galit
;  APPLICANT: Nemzer, Sergey
;  APPLICANT: Rosenberg, Avi
;  APPLICANT: Dahary, Dvir
;  APPLICANT: Cojocaru, Gad S.
;  APPLICANT: Akiva, Pinchas
;  APPLICANT: Wool, Assaf
;  APPLICANT: Pollock, Sarah
;  APPLICANT: Savitsky, Kinneret
;  APPLICANT: Bernstein, Jeanne
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING POLYPEPTIDES AND METHODS USING
;  TITLE OF INVENTION: SAME
;  FILE REFERENCE: 28487
;  CURRENT APPLICATION NUMBER: PCT/US05/02350
;  CURRENT FILING DATE: 2005-02-10
;  NUMBER OF SEQ ID NOS: 1155
;  SOFTWARE: Patentin version 3.3
; SEQ ID NO 272
;  LENGTH: 545
;  TYPE: PRT
;  ORGANISM: Homo sapiens
PCT-US05-02350-272
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  Query Match            19.7%;  Pred. No. 0.0006;  Length 545;
  Best Local Similarity   6.6%;  Score 139;  DB 1;
  Matches   85;  Conservative  59;  Mismatches 126;  Indels 162;  Gaps  19;

Qy    23 LEVPESVTGPW------------KGDVNLPCTYDPLQGYTQVLVKWLVQRGSDPVTIFLRDSSG 74
         : :|                    |:|                         |:| :
Db   145 IIIPCRVTDPQLVVTLHEKKGDVALPVPYDHQRGFSGI------------------ 182

Qy    75 DHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQVVRDKITTELR 134
         ::||                                             ::|
Db   183 -------FEDRSYICKTTIGD-------REVDSDAYY----VYRLQ 210

Qy   135 VQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQQARGSPPISYIW-YKQQTNNQ--EPIKVA 191
         | |: | |   ::        |   |:  : |  ::|:|            :: ||:
Db   211 VSSINVSVNAVQT-----VVRQGENITLMCIVIGNEVVNFEWTYPRKESGRLVEPVTDF 264

Qy   192 TL------STLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAP 244
         :|      |:||:     |||| :| :   |        ::::      :|
Db   265 LLDMPYIHIRSILHIPSAELEDSGTYTCNVTESVNDHQDEKAINITVVESG-YVRLLGEVG 323

Qy   245 TTMTYPLKAITSTVKQSWD--------WTTDMDGYLGETSAGPGKSLPVPFAIILIISLCCM 296
         | :| :  |      |          |:|: ||             |  | |      :
Db   324 TLQPAELIRSRTLQVVFEAYPPPTVLWFKD-NRTLGDSSAGE------------IALSTR 370

Qy   297 VVFTMAYI----MLCRKTSQQEH--------------VYEAARAHAREA 327
          |  :|:   | :::                       |
Db   371 NVSETRYVSELTLVRVKVAEAGHYTMRAFHEDAEVQLSFQLQINVPVRVLELSESHP--- 427

Qy   328 NDSGE-TMRVA-------IFASGC--------SSDEPTSQNLGNNYSDEP 361
         :|||   |:        ||          |:||
Db   428 -DSGEQTVRCRGRGMPQPNIIWSACRDLKRCPRELPPILLGNSSEEBSQLETNVTYWEEE 486

Qy   362 CIGQEYQIIAQI 373
          | ||: :    |
Db   487 ---QEFEVVSTL 495
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Search completed: March 2, 2005, 15:22:40
Job time : 33 secs

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: March 2, 2005, 15:09:10 ; Search time 24 Seconds
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Title: US-10-633-008-32
Perfect score: 2098
Sequence: 1 MGILLGLLLLGHLTVDTYGR.........LLDTVPLDYEFLATEGKSVC 399

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1500 summaries

Database :   Issued_Patents AA:*
                 1: /cgn2_6/ptcodata/1/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptcodata/1/iaa/5B_COMB.pep:*
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                 4: /cgn2_6/ptcodata/1/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptcodata/1/iaa/PCTUS_COMB.pep:*
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	ID	Description
1	1688	80.5	321	4	US-09-254-465A-2	Sequence 2, Appli
2	1688	80.5	321	4	US-09-953-499-2	Sequence 2, Appli
3	1547	73.7	306	4	US-09-369-247-63	Sequence 63, Appli
4	870	41.5	175	4	US-09-763-902B-6	Sequence 6, Appli
5	178.5	8.5	299	3	US-09-188-930-189	Sequence 189, App
6	178.5	8.5	299	3	US-09-188-930-331	Sequence 331, App
7	178.5	8.5	299	3	US-09-462-270-2	Sequence 2, Appli
8	178.5	8.5	299	4	US-09-254-465A-1	Sequence 1, Appli
9	178.5	8.5	299	4	US-09-312-283C-189	Sequence 189, App
10	178.5	8.5	299	4	US-09-312-283C-331	Sequence 331, App
11	178.5	8.5	299	4	US-09-907-794A-119	Sequence 119, App
12	178.5	8.5	299	4	US-09-905-125A-119	Sequence 119, App
13	178.5	8.5	299	4	US-09-902-775A-119	Sequence 119, App
14	178.5	8.5	299	4	US-09-397-243D-3	Sequence 3, Appli
15	178.5	8.5	299	4	US-09-906-700-119	Sequence 119, App
16	178.5	8.5	299	4	US-09-903-603A-119	Sequence 119, App
17	178.5	8.5	299	4	US-09-904-920A-119	Sequence 119, App
18	178.5	8.5	299	4	US-09-905-381A-119	Sequence 119, App
19	178.5	8.5	299	4	US-09-905-064-119	Sequence 119, App
20	178.5	8.5	299	4	US-09-906-618-119	Sequence 119, App
21	178.5	8.5	299	1	US-09-953-499-1	Sequence 1, Appli
22	178.5	8.5	319	1	US-08-597-495B-22	Sequence 22, Appl
23	177	8.4	319	3	US-09-068-051A-22	Sequence 22, Appl
24	177	8.4	319	4	US-09-336-536-67	Sequence 67, Appl
25	177	8.4	319	4	US-09-254-465A-6	Sequence 6, Appli
26	177	8.4	319	4	US-09-953-499-6	Sequence 6, Appli
27	176	8.4	270	4	US-09-254-465A-24	Sequence 24, Appl
28	176	8.4	270	4	US-09-953-499-24	Sequence 24, Appl
29	176	8.4	273	4	US-09-254-465A-26	Sequence 26, Appl
30	176	8.4	273	4	US-09-953-499-26	Sequence 26, Appl
31	172.5	8.2	316	4	US-09-397-243D-13	Sequence 13, Appl
32	169.5	8.1	260	4	US-09-254-465A-23	Sequence 23, Appl
33	169.5	8.1	260	4	US-09-953-499-23	Sequence 23, Appl
34	169.5	8.1	263	4	US-09-254-465A-25	Sequence 25, Appl
35	169.5	8.1	263	4	US-09-953-499-25	Sequence 25, Appl
36	167	8.0	300	4	US-09-254-465A-10	Sequence 10, Appl
37	167	8.0	300	4	US-09-953-499-10	Sequence 10, Appl
38	167	8.0	300	4	US-09-397-243D-12	Sequence 12, Appl
39	163.5	7.8	365	4	US-09-254-465A-32	Sequence 32, Appl
40	163.5	7.8	318	2	US-08-928-383B-2	Sequence 2, Appli
41	159	7.6	365	3	US-09-272-496-2	Sequence 2, Appli
42	159	7.6	365	2	US-08-899-634C-4	Sequence 2, Appli
43	159	7.6	365	2	US-08-899-634C-2	Sequence 2, Appli
44	159	7.6	365	3	US-09-060-051A-32	Sequence 2, Appli
45	159	7.6	383	3	US-09-949-016-11050	Sequence 14, Appl
46	159	7.6	466	3	US-09-949-016-6064	Sequence 24, Appl
47	151	7.2	1395	3	US-08-604-107A-8	Sequence 8, Appli
48	150	7.1	894	3	US-09-540-245A-15	Sequence 15, Appl
49	142.5	6.8	398	4	US-09-778-516-1	Sequence 4, Appli
50	142.5	6.8	561	3	US-09-949-016-10605	Sequence 24, Appl
51	140.5	6.7	365	3	US-09-949-016-10605	Sequence 23, Appl
52	140.5	6.7	365	2	US-08-928-383B-24	Sequence 24, Appl
53	140.5	6.7	383	2	US-08-928-383B-26	Sequence 26, Appl
54	140.5	6.7	1090	4	US-09-866-510-24	Sequence 4, Appli
55	139	6.6	1106	3	US-09-583-459A-2	Sequence 2, Appli
56	139	6.6	1106	1	US-08-180-195-2	Sequence 2, Appli
57	139	6.6	1106	1	US-08-160-917-2	Sequence 2, Appli
58	139	6.6	1106	1	US-08-477-329-2	Sequence 2, Appli
59	139	6.6	1106	2	US-09-475-458-2	Sequence 2, Appli
60	139	6.6	1106	2	US-08-460-510-2	Sequence 2, Appli
61	139	6.6	1106	2	US-08-460-490-2	Sequence 2, Appli
62	139	6.6	1106	2	US-08-460-400-2	Sequence 2, Appli
63	139	6.6	1106	2	US-08-980-400-2	Sequence 4, Appli
64	139	6.6	1106	3	US-08-462-728-4	Sequence 2, Appli
65	139	6.6	1106	3	US-09-583-449A-2	Sequence 2, Appli
66	139	6.6	1106	2	US-09-435-917-2	Sequence 2, Appli
67	139	6.6	1106	2	US-08-441-917-4	Sequence 2, Appli
68	139	6.6	1106	3	US-08-461-436-4	Sequence 4, Appli
69	139	6.6	1106	3	US-08-464-436-4	Sequence 4, Appli
70	139	6.6	1106	3	US-08-464-436-4	Sequence 2, Appli
71	139	6.6	1106	4	US-08-866-510-16	Sequence 16, Appl
72	139	6.6	1106	4	US-08-866-510-16	Sequence 18, Appl
73	139	6.6	1106	4	US-08-866-510-18	Sequence 20, Appl
74	139	6.6	1106	4	US-08-866-510-20	Sequence 22, Appl
75	139	6.6	1106	4	US-08-866-510-22	Sequence 2, Appli
76	139	6.6	1106	5	PCT-US92-00730-2	Sequence 2, Appli
77	138.5	6.6	310	4	US-09-907-794A-423	Sequence 423, App
78	138.5	6.6	310	4	US-09-905-125A-423	Sequence 423, App
79	138.5	6.6	310	4	US-09-902-775A-423	Sequence 423, App
80	138.5	6.6	310	4	US-09-906-700-423	Sequence 423, App
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82	138.5	6.6	310	4	US-09-904-920A-423	Sequence 423, App
83	138.5	6.6	310	4	US-09-905-381A-423	Sequence 423, App
84	138.5	6.6	310	4	US-09-905-064-423	Sequence 423, App
85	138.5	6.6	310	4	US-09-906-618-423	Sequence 423, App
86	138.5	6.6	360	4	US-09-907-794A-213	Sequence 213, App
87	138.5	6.6	360	4	US-09-905-125A-213	Sequence 213, App
88	138.5	6.6	360	4	US-09-902-775A-213	Sequence 213, App
89	138.5	6.6	360	4	US-09-906-700-213	Sequence 213, App
90	138	6.6	360	4	US-09-903-603A-213	Sequence 213, App
91	138	6.6	360	4	US-09-904-920A-213	Sequence 213, App
92	138	6.6	360	4	US-09-905-381A-213	Sequence 213, App
93	138	6.6	1059	4	US-09-905-064-213	Sequence 213, App
94	138	6.6	1059	4	US-09-906-618-213	Sequence 213, App
95	138	6.6	1059	4	US-09-902-775A-290	Sequence 290, App
96	138	6.6	1059	4	US-09-905-125A-290	Sequence 290, App
97	138	6.6	1059	4	US-09-906-700-290	Sequence 290, App
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103	138	6.6	1059	4	US-09-906-618-290	Sequence 290, App
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105	138	6.6	1119	4	US-09-905-125A-294	Sequence 294, App
106	138	6.6	1119	4	US-09-902-775A-294	Sequence 294, App
107	138	6.6	1119	4	US-09-906-700-294	Sequence 294, App
108	138	6.6	1119	4	US-09-903-603A-294	Sequence 294, App
109	138	6.6	1119	4	US-09-904-920A-294	Sequence 294, App
110	138	6.6	1119	4	US-09-909-064-294	Sequence 294, App
111	138	6.6	1119	4	US-09-905-381A-294	Sequence 294, App
112	138	6.6	1119	4	US-09-906-618-294	Sequence 294, App
113	137	6.5	398	4	US-09-778-510-6	Sequence 6, Appli
114	137	6.5	398	4	US-09-907-794A-84	Sequence 84, Appl
115	137	6.5	398	4	US-09-905-125A-84	Sequence 84, Appl
116	137	6.5	398	4	US-09-902-775A-84	Sequence 84, Appl
117	137	6.5	398	4	US-09-906-700-84	Sequence 84, Appl
118	137	6.5	398	4	US-09-903-603A-84	Sequence 84, Appl
119	137	6.5	398	4	US-09-904-920A-84	Sequence 84, Appl
120	137	6.5	398	4	US-09-909-064-84	Sequence 84, Appl
121	137	6.5	398	4	US-09-905-381A-84	Sequence 84, Appl
122	137	6.5	432	4	US-09-906-618-84	Sequence 84, Appl
123	137	6.5	450	4	US-09-778-510-2	Sequence 2, Appli
124	137	6.5	450	4	US-09-907-794A-320	Sequence 320, App
125	137	6.5	450	4	US-09-905-125A-320	Sequence 320, App
126	137	6.5	450	4	US-09-902-775A-320	Sequence 320, App
127	137	6.5	450	4	US-09-906-700-320	Sequence 320, App
128	137	6.5	450	4	US-09-903-603A-320	Sequence 320, App
129	137	6.5	450	4	US-09-904-920A-320	Sequence 320, App
130	137	6.5	450	4	US-09-909-064-320	Sequence 320, App
131	137	6.5	450	4	US-09-905-381A-320	Sequence 320, App
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134	136	6.4	249	4	US-09-336-536-42	Sequence 42, Appl
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136	135	6.4	193	3	US-08-759-628-4	Sequence 4, Appli
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138	134.5	6.4	440	4	US-09-944-457-61	Sequence 61, Appl
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142	133.5	6.4	467	3	US-09-046-736-2	Sequence 2, Appli
143	132.5	6.3	630	2	US-08-757-307B-14	Sequence 14, Appl
144	132.5	6.3	630	4	US-09-752-307B-14	Sequence 14, Appl
145	132.5	6.3	630	4	US-09-991-326-14	Sequence 14, Appl
146	131	6.3	4391	4	US-10-006-001A-2	Sequence 2, Appli
147	130	6.2	624	4	US-08-467-602-326	Sequence 326, App
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149	130	6.2	658	4	US-08-467-602-368	Sequence 368, App
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154	130	6.2	875	4	US-08-411-295F-295	Sequence 295, App
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156	130	6.2	888	4	US-08-411-295F-295	Sequence 295, App
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161	129	6.1	303	4	US-09-651-200-23	Sequence 23, Appl
162	129	6.1	303	4	US-09-441-411-20	Sequence 20, Appl
163	129	6.1	303	4	US-09-441-411-15	Sequence 15, Appl
164	129	6.1	309	2	US-08-456-104-4	Sequence 4, Appli
165	129	6.1	309	2	US-08-479-744A-23	Sequence 23, Appl
166	129	6.1	309	3	US-08-280-757B-23	Sequence 23, Appl
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168	129	6.1	309	3	US-08-702-525-21	Sequence 21, Appl
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170	129	6.1	309	4	US-09-667-135-33	Sequence 33, Appl
171	129	6.1	309	4	US-09-425-762-23	Sequence 23, Appl
172	129	6.1	309	4	US-09-837-867A-21	Sequence 21, Appl
173	129	6.1	309	4	US-09-206-132-4	Sequence 4, Appli
174	129	6.1	309	4	US-09-441-411-13	Sequence 13, Appl
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176	129	6.1	309	4	US-09-441-411-24	Sequence 24, Appl
177	129	6.1	309	5	US-09-425-516-23	Sequence 23, Appl
178	129	6.1	309	5	PCT-US95-02576-21	Sequence 21, Appl
179	129	6.1	314	3	US-08-205-697A-13	Sequence 13, Appl
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182	129	6.1	314	4	US-09-441-411-14	Sequence 14, Appl
183	129	6.1	314	4	US-09-837-867A-13	Sequence 13, Appl
184	129	6.1	314	5	US-09-441-411-19	Sequence 19, Appl
185	129	6.1	356	4	PCT-US95-02576-13	Sequence 13, Appl
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187	129	6.1	356	4	US-09-441-411-11	Sequence 11, Appl
188	129	6.1	356	4	US-09-441-411-12	Sequence 12, Appl
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190	129	6.1	1248	3	US-09-949-016-10596	Sequence 10596, A
191	128.5	6.1	613	4	US-08-470-335-230	Sequence 230, App
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200	128.5	6.1	830	4	US-08-470-335-231	Sequence 231, App
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205	128.5	6.1	864	4	US-08-467-602-372	Sequence 372, App
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220	128	6.1	479	4	US-09-949-016-6278	Sequence 6278, Ap
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228	127	6.1	465	3	US-09-707-802-5	Sequence 5, Appli
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244	122.5	5.8	612	3	US-09-991-326-11	Sequence 11, Appl
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246	122.5	5.8	738	4	US-09-336-536-73	Sequence 73, Appl

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249	122	5.8	604	3	US-08-467-602-318	Sequence 318, App
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252	122	5.8	611	3	US-09-707-802-10	Sequence 10, Appl
253	122	5.8	611	3	US-09-991-326-10	Sequence 10, Appl
254	122	5.8	638	4	US-08-467-602-360	Sequence 360, App
255	122	5.8	638	3	US-08-411-295F-286	Sequence 286, App
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275	120.5	5.7	658	4	US-08-467-602-305	Sequence 305, App
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323	119	5.7	635	3	US-08-411-295F-157	Sequence 157, App
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349	119	5.7	884	4	US-08-467-602-315	Sequence 315, App
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364	119	5.7	965	3	US-08-470-335-245	Sequence 245, App
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371	118	5.6	547	2	US-08-473-981A-6	Sequence 6, Appli
372	118	5.6	758	3	US-08-874-678-1	Sequence 1, Appl
373	118	5.6	758	3	US-09-051-363-24	Sequence 24, Appl
374	118	5.6	758	1	US-09-348-886-1	Sequence 1, Appl
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380	117.5	5.6	1338	3	US-08-414-657D-46	Sequence 46, Appl
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430	116.5	5.6	652	3	US-08-842-248A-4	Sequence 4, Appli
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447	116	5.6	375	4	US-08-467-602-242	Sequence 242, App
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672	107.5	5.1	572	4	US-08-411-295F-161	Sequence 161, App
673	107.5	5.1	572	4	US-08-467-602-234	Sequence 234, App
674	107.5	5.1	619	4	US-08-411-295F-233	Sequence 233, App
675	107.5	5.1	619	4	US-08-411-295F-159	Sequence 159, App
676	107.5	5.1	731	1	US-07-921-807B-5	Sequence 5, Appli
677	107.5	5.1	731	4	US-08-441-944A-5	Sequence 5, Appli
678	107.5	5.1	731	3	US-08-439-992A-3	Sequence 3, Appli
679	107.5	5.1	1297	3	US-08-540-245A-17	Sequence 17, Appl
680	107.5	5.1	1297	3	US-08-340-011-5	Sequence 5, Appli
681	107.5	5.1	1311	4	US-08-901-710-5	Sequence 5, Appli
682	107	5.1	1311	2	US-08-169-079-5	Sequence 5, Appli
683	107	5.1	1311	2	US-08-642-406A-22	Sequence 22, Appl
684	107	5.1	624	3	US-09-199-534-22	Sequence 22, Appl

685	107	5.1	624	4	US-09-199-554-22	Sequence 22, Appl
686	107	5.1	729	4	US-07-640-029-3	Sequence 3, Appli
687	106.5	5.1	240	2	US-07-956-399-2	Sequence 2, Appli
688	106.5	5.1	395	4	US-08-467-602-227	Sequence 227, App
689	106.5	5.1	395	4	US-08-411-295F-153	Sequence 153, App
690	106.5	5.1	429	4	US-08-467-602-269	Sequence 269, App
691	106.5	5.1	429	4	US-08-411-295F-195	Sequence 195, App
692	106.5	5.1	612	4	US-08-467-602-228	Sequence 228, App
693	106.5	5.1	612	4	US-08-411-295F-154	Sequence 154, App
694	106.5	5.1	646	4	US-08-467-602-270	Sequence 270, App
695	106.5	5.1	646	4	US-08-411-295F-196	Sequence 196, App
696	106.5	5.1	659	4	US-08-467-602-229	Sequence 229, App
697	106.5	5.1	659	4	US-08-411-295F-155	Sequence 155, App
698	106.5	5.1	693	4	US-08-467-602-271	Sequence 271, App
699	106.5	5.1	693	4	US-08-411-295F-197	Sequence 197, App
700	106.5	5.1	733	1	US-07-640-029-4	Sequence 4, Appli
701	106.5	5.1	733	1	US-07-921-807B-6	Sequence 6, Appli
702	106.5	5.1	733	1	US-08-411-944A-6	Sequence 6, Appli
703	106.5	5.1	733	3	US-08-439-992A-4	Sequence 4, Appli
704	106.5	5.1	801	1	US-09-383-630-6	Sequence 6, Appli
705	106.5	5.1	817	1	US-07-640-029-2	Sequence 2, Appli
706	106.5	5.1	820	1	US-07-921-807B-3	Sequence 3, Appli
707	106.5	5.1	820	1	US-08-441-944A-3	Sequence 3, Appli
708	106.5	5.1	820	3	US-08-439-992A-1	Sequence 1, Appli
709	106.5	5.1	822	1	US-07-997-133-1	Sequence 1, Appli
710	106.5	5.1	822	1	US-08-411-944A-4	Sequence 4, Appli
711	106.5	5.1	822	1	US-07-921-807B-4	Sequence 4, Appli
712	106.5	5.1	822	1	US-08-499-296-2	Sequence 2, Appli
713	106.5	5.1	822	2	US-07-921-807B-12	Sequence 12, Appli
714	106.5	5.1	822	2	US-08-441-944A-12	Sequence 12, Appli
715	106.5	5.1	822	3	US-08-439-992A-2	Sequence 2, Appli
716	106.5	5.1	869	1	US-08-451-822A-12	Sequence 12, Appli
717	106.5	5.1	1474	4	US-09-323-430-12	Sequence 12, Appli
718	106	5.1	1953	4	US-09-715-249-8	Sequence 8, Appli
719	106.5	5.1	246	1	US-09-677-046A-4	Sequence 4, Appli
720	105.5	5.0	324	4	US-09-917-254-92	Sequence 92, Appl
721	105.5	5.0	324	4	US-07-843-125-11	Sequence 11, Appl
722	105.5	5.0	351	5	US-09-910-174B-6	Sequence 6, Appli
723	105.5	5.0	408	3	US-09-620-461-6	Sequence 6, Appli
724	105.5	5.0	589	2	PCT-US93-05703-2	Sequence 2, Appli
725	105.5	5.0	609	4	US-09-724-864-62	Sequence 62, Appli
726	105.5	5.0	609	4	US-09-949-016-7747	Sequence 7747, Appl
727	105.5	5.0	609	4	US-09-949-016-7748	Sequence 7748, Ap
728	105.5	5.0	609	4	US-09-949-016-7749	Sequence 7749, Ap
729	105.5	5.0	609	4	US-09-949-016-7750	Sequence 7750, Ap
730	105.5	5.0	609	4	US-09-949-016-7751	Sequence 7751, Ap
731	105.5	5.0	609	4	US-09-949-016-7752	Sequence 7752, Ap
732	105.5	5.0	609	4	US-09-949-016-7753	Sequence 7753, Ap
733	105.5	5.0	651	4	US-09-270-767-44877	Sequence 44877, A
734	105.5	5.0	1509	4	US-09-949-016-7754	Sequence 7754, Ap
735	105	5.0	336	4	US-09-677-046A-2	Sequence 2, Appl
736	105	5.0	336	4	US-09-949-016-7715	Sequence 7715, Ap
737	105	5.0	540	2	US-08-724-394A-4	Sequence 4, Appli
738	105	5.0	828	1	US-08-261-304-2	Sequence 2, Appli
739	105	5.0	1461	4	US-09-976-594-531	Sequence 531, Appl
740	104.5	5.0	1503	4	US-09-677-046A-6	Sequence 6, Appli
741	104	5.0	386	4	US-08-467-602-218	Sequence 218, Appl
742	104	5.0	386	4	US-08-411-295F-144	Sequence 144, App
743	104	5.0	420	4	US-08-847-743B-29	Sequence 29, Appli
744	104	5.0	420	1	US-08-456-201-29	Sequence 29, Appli
745	104	5.0	420	4	US-08-456-241-29	Sequence 29, Appli
746	104	5.0	420	4	US-08-467-602-260	Sequence 260, Appl
747	104	5.0	420	4	US-08-411-295F-186	Sequence 186, App
748	104	5.0	420	5	PCT-US92-04295A-29	Sequence 29, Appl
749	104	5.0	603	4	US-08-467-602-216	Sequence 216, Appl
750	104	5.0	603	4	US-08-411-295F-142	Sequence 142, App
751	104	5.0	637	1	US-07-847-743B-28	Sequence 28, Appli
752	104	5.0	637	4	US-08-411-295F-28	Sequence 28, Appli
753	104	5.0	637	2	US-08-456-201-28	Sequence 28, Appli
754	104	5.0	637	4	US-08-456-241-28	Sequence 28, Appli
755	104	5.0	637	4	US-08-467-602-258	Sequence 258, Appl
756	104	5.0	637	5	US-08-411-295F-184	Sequence 184, App
757	104	5.0	650	4	PCT-US92-04295A-28	Sequence 28, Appl

758	104	5.0	650	4	US-08-411-295F-143	Sequence 143, App
759	104	5.0	668	1	US-08-232-538-13	Sequence 13, Appl
760	104	5.0	668	2	US-08-786-164-13	Sequence 13, Appl
761	104	5.0	684	4	US-08-467-602-259	Sequence 259, Appl
762	104	5.0	684	4	US-08-411-295F-185	Sequence 185, App
763	104	5.0	764	3	US-09-142-956B-14	Sequence 14, Appl
764	104	5.0	767	2	US-08-874-678-2	Sequence 2, Appli
765	104	5.0	767	3	US-08-643-839-2	Sequence 2, Appli
766	104	5.0	767	4	US-09-348-886-2	Sequence 2, Appli
767	104	5.0	788	1	US-08-786-164-15	Sequence 15, Appl
768	104	5.0	788	2	US-08-232-533-15	Sequence 15, Appl
769	103.5	5.0	1356	1	US-08-810-116-8	Sequence 8, Appl
770	103.5	5.0	1356	2	US-09-098-707A-2	Sequence 2, Appl
771	104	5.0	1356	3	US-09-483-539-2	Sequence 2, Appl
772	104	5.0	1356	3	US-09-949-016-6198	Sequence 6198, App
773	104	5.0	1356	4	US-09-949-016-9853	Sequence 9853, App
774	104	4.9	1456	1	US-08-408-095-31	Sequence 31, Appl
775	103.5	4.9	501	2	US-09-949-016-7565	Sequence 7565, Ap
776	103.5	4.9	640	4	US-09-540-245A-8	Sequence 8, Appli
777	103.5	4.9	1381	4	US-09-540-245A-16	Sequence 16, Appl
778	103.5	4.9	1651	3	US-08-235-838-14	Sequence 14, Appl
779	103	4.9	637	2	US-08-465-473B-14	Sequence 14, Appl
780	103	4.9	395	4	US-08-467-602-292	Sequence 292, App
781	103	4.9	612	4	US-08-411-295F-218	Sequence 218, App
782	103	4.9	612	4	US-08-467-602-291	Sequence 291, App
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784	103	4.9	637	2	US-08-467-602-290	Sequence 290, App
785	103	4.9	657	4	US-08-411-295F-216	Sequence 216, App
786	103	4.9	659	4	US-08-411-295F-217	Sequence 217, App
787	103	4.9	659	4	US-08-467-602-292	Sequence 292, App
788	103	4.9	1140	3	US-08-579-698B-8	Sequence 8, Appl
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790	102.5	4.9	326	1	PCT-US95-04353-6	Sequence 6, Appl
791	102.5	4.9	599	1	US-09-907-794A-292	Sequence 292, App
792	102.5	4.9	640	4	US-09-905-125A-292	Sequence 292, App
793	102.5	4.9	640	4	US-09-902-775A-292	Sequence 292, App
794	102.5	4.9	640	4	US-09-906-700-292	Sequence 292, App
795	102.5	4.9	640	4	US-09-906-618-292	Sequence 292, App
796	102.5	4.9	640	4	US-09-903-603A-292	Sequence 292, App
797	102.5	4.9	640	4	US-09-903-603A-292	Sequence 292, App
798	102.5	4.9	640	4	US-09-909-064-292	Sequence 292, App
799	102.5	4.9	640	4	US-09-905-381A-292	Sequence 292, App
800	102.5	4.9	640	4	US-09-906-618-292	Sequence 292, App
801	102.5	4.9	640	2	US-09-918-914-1	Sequence 1, Appli
802	102.5	4.9	1184	2	US-08-996-083-3	Sequence 3, Appli
803	102	4.9	319	1	US-09-910-174B-12	Sequence 12, Appl
804	102	4.9	319	4	US-09-910-174B-12	Sequence 12, Appl
805	102	4.9	347	1	US-09-620-461-12	Sequence 12, Appl
806	102	4.9	357	4	US-09-620-461-14	Sequence 14, Appl
807	102	4.9	523	4	US-09-910-174B-11	Sequence 11, Appl
808	102	4.9	523	4	US-09-620-461-11	Sequence 11, Appl
809	102	4.9	626	4	US-09-949-016-6213	Sequence 6213, Ap
810	102	4.9	642	1	US-08-217-299-1	Sequence 1, Appli
811	102	4.9	664	2	US-09-949-016-7850	Sequence 7850, Appl
812	102	4.9	698	2	US-08-602-725-36	Sequence 36, Appl
813	102	4.9	702	4	US-09-949-016-6484	Sequence 6484, Ap
814	102	4.9	734	2	US-08-389-453A-17	Sequence 17, Appl
815	102	4.9	734	2	US-08-987-867A-17	Sequence 17, Appl
816	102	4.9	740	4	US-09-949-016-8168	Sequence 8168, Ap
817	101.5	4.8	361	1	US-08-467-602-248	Sequence 248, App
818	101.5	4.8	361	4	US-08-411-295F-174	Sequence 174, App
819	101.5	4.8	456	2	US-09-949-016-7564	Sequence 7564, Ap
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821	101.5	4.8	625	4	US-08-467-602-250	Sequence 250, App
822	101.5	4.8	625	4	US-08-411-295F-176	Sequence 176, App
823	101.5	4.8	816	4	US-09-949-016-10904	Sequence 10904, A
824	101.5	4.8	1260	3	US-08-506-296B-21	Sequence 21, Appl
825	101.5	4.8	816	4	US-09-949-016-10904	Sequence 10904, A
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827	101	4.8	318	3	5233394-11	Patent No. 5233394
828	101	4.8	318	6	5233394-11	Patent No. 5233394
829	101	4.8	394	3	US-08-466-368-2	Sequence 2, Appli
830	101	4.8	394	4	US-08-328-500-2	Sequence 2, Appli

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831	101	4.8	458	3	US-09-517-605-3 — Sequence 3, Appli
832	101	4.8	890	3	US-08-445-640-2 — Sequence 2, Appli
833	101	4.8	890	3	US-08-170-558-2 — Sequence 2, Appli
834	101	4.8	890	3	US-08-447-314-2 — Sequence 2, Appli
835	101	4.8	890	4	US-09-445-461-2 — Sequence 2, Appli
836	101	4.8	890	4	US-09-223-490-2 — Sequence 2, Appli
837	101	4.8	890	4	US-08-286-305A-1 — Sequence 1, Appli
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839	101	4.8	911	2	US-08-440-816A-1 — Sequence 1, Appli
840	101	4.8	911	3	US-09-417-381A-1 — Sequence 1, Appli
841	100.5	4.8	304	3	US-08-862-124-14 — Sequence 14, Appl
842	100.5	4.8	386	4	US-08-467-602-281 — Sequence 281, Appl
843	100.5	4.8	386	4	US-08-411-295F-207 — Sequence 207, App
844	100.5	4.8	455	4	US-09-949-016-6949 — Sequence 6949, Ap
845	100.5	4.8	455	4	US-09-667-135-29 — Sequence 29, Appl
846	100.5	4.8	603	4	US-08-467-602-279 — Sequence 279, App
847	100.5	4.8	603	4	US-08-411-295F-205 — Sequence 205, Appl
848	100.5	4.8	650	4	US-08-467-602-280 — Sequence 280, App
849	100.5	4.8	650	3	US-08-411-295F-206 — Sequence 206, Appl
850	100.5	4.8	802	3	US-09-173-151A-33 — Sequence 33, Appl
851	100.5	4.8	63	4	US-09-397-243D-8 — Sequence 8, Appl
852	100	4.8	63	4	US-09-397-243D-10 — Sequence 10, Appl
853	100	4.8	124	3	US-08-858-644A-28 — Sequence 28, Appl
854	100	4.8	124	4	US-10-274-978-29 — Sequence 29, Appl
855	100	4.8	322	4	US-09-667-263-29 — Sequence 29, Appl
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857	100	4.8	322	4	US-09-910-174B-29 — Sequence 29, Appl
858	100	4.8	323	4	US-09-620-461-29 — Sequence 29, Appl
859	100	4.8	323	4	US-09-651-200-21 — Sequence 21, Appl
860	100	4.8	323	4	US-09-441-411-22 — Sequence 22, Appli
861	100	4.8	323	5	PCT-US94-09642-2 — Sequence 2, Appli
862	100	4.8	329	2	US-08-456-104-2 — Sequence 2, Appli
863	100	4.8	329	2	US-09-101-624-2 — Sequence 2, Appli
864	100	4.8	329	2	US-08-479-744A-2 — Sequence 2, Appli
865	100	4.8	329	3	US-08-280-757B-2 — Sequence 2, Appl
866	100	4.8	329	3	US-08-205-697A-23 — Sequence 23, Appl
867	100	4.8	329	3	US-08-702-525-23 — Sequence 23, Appl
868	100	4.8	329	4	US-08-403-253A-4 — Sequence 4, Appl
869	100	4.8	329	4	US-09-651-200-19 — Sequence 19, Appl
870	100	4.8	329	4	US-09-667-135-32 — Sequence 32, Appl
871	100	4.8	329	4	US-08-435-816A-4 — Sequence 4, Appl
872	100	4.8	329	4	US-09-425-762-2 — Sequence 2, Appl
873	100	4.8	329	4	US-09-837-867A-23 — Sequence 23, Appli
874	100	4.8	329	4	US-09-441-411-26 — Sequence 26, Appli
875	100	4.8	329	4	US-09-206-132-2 — Sequence 2, Appli
876	100	4.8	329	4	US-09-425-516-2 — Sequence 2, Appli
877	100	4.8	329	5	PCT-US95-02576-23 — Sequence 23, Appl
878	100	4.8	372	4	PCT-US95-016-11132 — Sequence 11132, A
879	100	4.8	373	4	US-09-949-016-10485 — Sequence 10485, A
880	100	4.8	458	4	US-10-092-138A-25 — Sequence 25, Appl
881	100	4.8	530	4	US-08-840-713-2 — Sequence 2, Appl
882	100	4.8	584	4	US-09-910-174B-16 — Sequence 16, Appl
883	100	4.8	584	4	US-09-620-461-16 — Sequence 16, Appl
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886	99.5	4.8	365	4	US-09-949-016-6907 — Sequence 6907, Ap
887	99.5	4.8	391	4	US-09-949-016-7325 — Sequence 7325, Ap
888	99.5	4.8	596	2	US-08-752-307B-13 — Sequence 13, Appl
889	99.5	4.8	596	3	US-09-707-802-13 — Sequence 13, Appl
890	99.5	4.8	596	3	US-09-991-326-13 — Sequence 13, Appl
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893	99	4.8	341	1	US-09-336-536-29 — Sequence 29, Appl
894	99	4.8	352	4	US-08-467-602-239 — Sequence 239, Appl
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896	99	4.8	370	4	US-09-336-536-28 — Sequence 28, Appl
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898	99	4.8	388	3	US-08-445-640-6 — Sequence 6, Appli
899	99	4.8	388	3	US-08-447-314-6 — Sequence 6, Appli
900	99	4.7	388	4	US-09-223-490-6 — Sequence 6, Appli
901	99	4.7	388	4	US-08-445-461-6 — Sequence 6, Appli
902	99	4.7	394	6	5223418-2 — Patent No. 5223418-2
903	99	4.7	394	6	5223418 — Patent No. 5223418
904	99	4.7	458	3	US-09-039-555B-15 — Sequence 15, Appl
905	99	4.7	569	4	US-08-467-602-237 — Sequence 237, App
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908	99	4.7	616	4	US-08-411-295F-164 — Sequence 164, App
909	99	4.7	645	1	US-07-847-743B-27 — Sequence 27, Appl
910	99	4.7	645	1	US-08-456-201-27 — Sequence 27, Appl
911	99	4.7	645	1	US-09-097-681-3 — Sequence 3, Appli
912	99	4.7	645	1	PCT-US92-04295A-27 — Sequence 27, Appli
913	99	4.7	645	1	US-09-753-007A-32 — Sequence 32, Appli
914	99	4.7	645	1	US-09-398-496-32 — Sequence 32, Appl
915	99	4.7	647	3	US-09-101-544-93 — Sequence 93, Appl
916	99	4.7	647	3	US-09-020-880-93 — Sequence 93, Appl
917	99	4.7	645	3	US-09-398-496-10 — Sequence 10, Appl
918	99	4.7	645	3	US-08-456-241-27 — Sequence 27, Appl
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920	99	4.7	645	1	US-08-428-926-4 — Sequence 4, Appli
921	99	4.7	645	1	US-08-428-298-4 — Sequence 4, Appli
922	99	4.7	645	3	US-08-428-927-4 — Sequence 4, Appli
923	99	4.7	647	3	US-09-398-496-32 — Sequence 32, Appl
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925	99	4.7	732	1	US-08-456-201-9 — Sequence 9, Appli
926	99	4.7	732	2	US-08-456-241-9 — Sequence 9, Appli
927	99	4.7	732	2	PCT-US92-04295A-9 — Sequence 9, Appli
928	99	4.7	806	3	US-08-193-829B-5 — Sequence 5, Appli
929	99	4.7	806	2	US-08-443-861-5 — Sequence 5, Appli
930	99	4.7	1367	3	US-08-193-829B-5 — Sequence 5, Appli
931	99	4.7	1367	1	US-07-813-593-4 — Sequence 4, Appli
932	99	4.7	1367	1	US-07-977-451-6 — Sequence 6, Appli
933	99	4.7	1367	1	US-08-252-517-6 — Sequence 6, Appli
934	99	4.7	1367	1	US-08-601-891-6 — Sequence 6, Appli
935	99	4.7	1367	1	US-07-906-397A-6 — Sequence 6, Appli
936	99	4.7	1367	2	US-09-021-324-6 — Sequence 6, Appli
937	99	4.7	1367	2	US-09-872-136B-6 — Sequence 6, Appli
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939	99	4.7	1367	2	PCT-US92-05450-4 — Sequence 4, Appli
940	99	4.7	1367	2	PCT-US92-02750-8 — Sequence 8, Appli
941	99	4.7	1367	2	US-08-443-861-5 — Sequence 5, Appli
942	99	4.7	1367	2	PCT-US92-04295A-9 — Sequence 9, Appli
943	98.5	4.7	1367	2	US-08-193-829B-5 — Sequence 5, Appli
944	98	4.7	434	2	US-08-720-420A-120 — Sequence 120, App
945	98	4.7	434	2	US-08-487-1113D-120 — Sequence 120, App
946	98	4.7	240	4	US-09-270-767-32134 — Sequence 32134, A
947	98	4.7	240	1	US-09-270-767-47351 — Sequence 47351, A
948	98	4.7	243	3	US-08-230-843-4 — Sequence 4, Appli
949	98	4.7	246	1	US-08-636-936-4 — Sequence 4, Appli
950	98	4.7	246	4	US-09-336-536-31 — Sequence 31, Appli
951	98	4.7	295	6	5223394-9 — Patent No. 5223394-9
952	98	4.7	295	6	5223394-9 — Patent No. 5223394
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954	98	4.7	874	2	US-08-456-647B-6 — Sequence 6, Appli
955	98	4.7	880	3	US-08-170-558-10 — Sequence 10, Appli
956	98	4.7	880	3	US-08-447-314-10 — Sequence 10, Appli
957	98	4.7	880	3	US-08-445-640-10 — Sequence 10, Appli
958	98	4.7	880	3	US-09-223-490-10 — Sequence 10, Appli
959	97.5	4.6	97	4	US-10-274-978-28 — Sequence 28, Appl
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961	97.5	4.6	97	4	US-09-949-016-8483 — Sequence 8483, Ap
962	97.5	4.6	246	1	US-09-197-834-7 — Sequence 7, Appli
963	97.5	4.6	332	2	US-08-724-394A-6 — Sequence 6, Appli
964	97.5	4.6	342	2	US-09-949-016-8483 — Sequence 8483, Ap
965	97.5	4.6	477	2	US-08-286-846A-4 — Sequence 4, Appli
966	97.5	4.6	477	2	US-08-457-880A-4 — Sequence 4, Appli
967	97.5	4.6	477	2	US-08-444-622A-4 — Sequence 4, Appli
968	97.5	4.6	477	3	US-08-942-562-4 — Sequence 4, Appli
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970	97.5	4.6	560	4	US-09-949-016-8293 — Sequence 8293, Ap
971	97.5	4.6	477	4	US-09-156-923-4 — Sequence 4, Appli
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973	97.5	4.6	822	2	US-08-359-705B-2 — Sequence 2, Appli
974	97.5	4.6	822	2	US-08-457-880A-2 — Sequence 2, Appli
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981	97.5	4.6	847	2	US-08-440-816A-5	Sequence 5, Appli
982	97.5	4.6	847	3	US-09-417-381A-5	Sequence 5, Appli
983	97	4.6	340	4	US-09-188-930-184	Sequence 184, App
984	97	4.6	340	4	US-09-312-283C-184	Sequence 184, App
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987	97	4.6	398	4	US-09-218-950A-29	Sequence 29, Appl
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990	97	4.6	402	4	US-09-157-408-1	Sequence 1, Appli
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992	97	4.6	458	4	US-08-328-500-9	Sequence 9, Appli
993	97	4.6	462	4	US-08-466-368-4	Sequence 4, Appli
994	97	4.6	462	2	US-08-394-388A-6	Sequence 6, Appli
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996	97	4.6	532	2	US-08-218-950-5	Sequence 5, Appli
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1067	94	4.5	422	2	US-08-469-526A-170	Sequence 170, App
1068	94	4.5	422	1	US-08-469-660-170	Sequence 170, App
1069	94	4.5	422	1	US-08-341-018-72	Sequence 72, Appl
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1076	94	4.5	422	2	US-08-734-591A-170	Sequence 170, App
1077	94	4.5	422	3	US-08-469-660-170	Sequence 170, App
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1079	94	4.5	422	3	US-08-470-335-170	Sequence 170, App
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1081	94	4.5	422	1	US-08-734-664A-170	Sequence 170, App
1082	94	4.5	422	3	US-08-470-339-170	Sequence 170, App
1083	94	4.5	422	4	US-08-454-564-4	Sequence 4, Appli
1084	94	4.5	422	3	US-08-411-295F-170	Sequence 170, App
1085	94	4.5	422	4	US-08-411-295F-66	Sequence 66, Appl
1086	94	4.5	422	4	US-08-411-295F-65	Sequence 65, Appl
1087	94	4.5	422	5	US-08-470-339-170	Sequence 170, App
1088	94	4.5	422	5	US-08-445-461-12	Sequence 12, Appl
1089	94	4.5	422	1	US-08-467-602-170	Sequence 170, App
1090	94	4.5	422	6	PCT-US95-06846A-170	Sequence 170, App
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1092	94	4.5	458	6	5223394-7	Patent No. 5223394
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1096	93.5	4.5	259	3	US-09-560-639-11	Sequence 11, Appl
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1098	93.5	4.5	388	1	US-08-445-640-12	Sequence 12, Appl
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1103	93.5	4.5	434	3	US-09-223-490-12	Sequence 12, Appl
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1107	93.5	4.5	479	4	US-08-411-295F-254	Sequence 254, App
1108	93.5	4.5	458	4	US-09-773-877B-26	Sequence 26, Appl
1109	93.5	4.5	479	4	US-08-467-602-370	Sequence 370, App
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1113	93	4.4	560	3	US-08-470-335-194	Sequence 194, App
1114	93	4.4	560	3	US-08-470-335-194	Sequence 194, App
1115	93	4.4	560	4	US-08-470-339-194	Sequence 194, App
1116	93	4.4	560	3	US-08-467-602-388	Sequence 388, App
1117	93	4.4	560	4	US-08-411-295F-51	Sequence 51, Appl
1118	93	4.4	560	4	US-08-411-295F-96	Sequence 96, Appl
1119	93	4.4	581	2	US-08-724-394A-3	Sequence 3, Appli
1120	93	4.4	741	4	US-09-585-858-11	Sequence 11, Appl
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1125	92.5	4.4	309	4	US-09-667-857-392	Sequence 392, Appl
1126	92.5	4.4	329	4	US-09-651-200-18	Sequence 18, Appli
1127	92.5	4.4	329	4	US-09-303-040-6	Sequence 6, Appli
1128	92.5	4.4	424	6	5169835-6	Patent No. 5169835
1129	92.5	4.4	424	6	5169835-6	Patent No. 5169835
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1131	92.5	4.4	426	1	PCT-US95-13795-2	Sequence 2, Appli
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1134	92.5	4.4	746	3	US-09-312-157-4	Sequence 4, Appli
1135	92.5	4.4	746	4	US-09-717-888-4	Sequence 4, Appli
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1143	92	4.4	302	1	US-08-121-054C-30	Sequence 30, Appl
1144	92	4.4	302	3	US-09-539-436-18	Sequence 18, Appl
1145	92	4.4	302	3	US-09-539-436-30	Sequence 30, Appl
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1154	92	4.4	422	4	US-08-470-339-188	Sequence 188, App
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1156	92	4.4	422	4	US-08-467-602-324	Sequence 324, App
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1160	92	4.4	456	3	US-08-470-335-246	Sequence 246, App
1161	92	4.4	456	4	US-08-467-602-303	Sequence 303, App
1162	92	4.4	456	4	US-08-467-602-366	Sequence 366, App
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1169	92	4.4	459	4	US-08-411-295F-288	Sequence 288, App
1170	92	4.4	479	4	US-08-467-602-307	Sequence 307, App
1171	92	4.4	479	4	US-08-411-295F-233	Sequence 233, App
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1173	92	4.4	493	4	US-08-411-295F-271	Sequence 271, App
1174	92	4.4	493	4	US-08-467-602-341	Sequence 341, App
1175	92	4.4	493	4	US-08-411-295F-267	Sequence 267, App
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1181	92	4.4	652	1	US-08-471-570-10	Sequence 10, Appli
1182	92	4.4	2491	4	US-09-207-363-1	Sequence 1, Appli
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1196	91.5	4.4	576	5	PCT-US96-08899-4	Sequence 4, Appli
1197	91.5	4.4	643	5	PCT-US93-00031-19	Sequence 19, Appl
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1211	91	4.3	405	4	US-09-397-243D-11	Sequence 11, Appl
1212	91	4.3	405	4	US-09-798-689-21	Sequence 21, Appl
1213	91	4.3	477	2	US-08-467-602-384	Sequence 384, App
1214	91	4.3	477	2	US-08-432-016-3	Sequence 3, Appli
1215	91	4.3	477	3	US-09-684-594-3	Sequence 3, Appli
1216	91	4.3	771	3	US-09-434-000A-8	Sequence 8, Appli
1217	91.5	4.4	771	3	US-09-312-157-8	Sequence 8, Appli
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1237	90	4.3	288	4	US-09-651-200-14	Sequence 14, Appl
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1258	90	4.3	582	4	US-09-736-457-334	Sequence 334, App
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1260	90	4.3	582	4	US-09-671-325-334	Sequence 334, App
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1264	90	4.3	821	2	US-08-451-822A-13	Sequence 13, Appl
1265	90	4.3	821	3	US-08-323-430-13	Sequence 13, Appl
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1273	89.5	4.3	597	4	US-09-746-311B-381	Sequence 381, App
1274	89.5	4.3	2315	4	US-09-543-681A-5434	Sequence 5434, Ap
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1276	89	4.2	287	4	US-09-800-729-114	Sequence 114, Appl
1277	89	4.2	287	4	US-09-800-729-153	Sequence 153, App
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1279	89	4.2	342	4	US-09-684-708A-27	Sequence 27, Appli
1280	89	4.2	466	2	US-08-432-016-4	Sequence 4, Appli
1281	89	4.2	466	2	US-08-684-594-4	Sequence 4, Appli
1282	89	4.2	583	2	US-08-432-016-2	Sequence 2, Appli
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1287	89	4.2	615	3	US-08-985-950-18	Sequence 18, Appl
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1289	89	4.2	615	3	US-08-546-049-18	Sequence 18, Appl
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1292	89	4.2	769	1	US-08-471-570-8	Sequence 8, Appli
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1324	88	4.2	787	2	US-09-453-702A-110	Sequence 110, App
1325	88	4.2	787	3	US-09-099-639-110	Sequence 110, App
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1337	87	4.1	382	4	US-08-467-602-382	Sequence 382, App
1338	87	4.1	535	4	US-08-983-035A-38	Sequence 38, Appl
1339	87	4.1	653	4	US-09-520-781-10	Sequence 10, Appl
1340	87	4.1	666	3	US-09-423-439-51	Sequence 51, Appl
1341	87	4.1	668	3	US-09-173-151A-35	Sequence 35, Appl
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1343	86.5	4.1	218	5	PCT-US94-14106-57	Sequence 57, Appl
1344	86.5	4.1	230	3	US-09-485-737B-102	Sequence 102, App
1345	86.5	4.1	230	4	US-10-071-485-102	Sequence 102, App
1346	86.5	4.1	669	3	US-10-071-035-264	Sequence 264, App
1347	86.5	4.1	826	3	US-09-877-730-16	Sequence 16, Appl
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1355	86.5	4.1	894	3	US-08-223-490-34	Sequence 34, Appl
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1362	86.5	4.1	1069	4	US-08-452-052-2	Sequence 2, Appli
1363	86.5	4.1	1072	4	US-09-652-501-2	Sequence 2, Appli
1364	86.5	4.1	1150	4	US-09-877-730-18	Sequence 18, Appl
1365	86.5	4.1	1363	4	US-09-375-248-19	Sequence 19, Appl
1366	86	4.1	241	3	US-08-341-011-54	Sequence 54, Appl
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1368	86	4.1	241	3	US-08-470-339-195	Sequence 195, App
1369	86	4.1	241	4	US-08-467-602-389	Sequence 389, App
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1373	86	4.1	398	2	US-09-091-519-2	Sequence 2, Appli
1374	86	4.1	398	3	US-08-442-043A-2	Sequence 2, Appli
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1378	86	4.1	398	4	US-08-406-824A-8	Sequence 8, Appli
1379	86	4.1	398	5	US-09-921-667-8	Sequence 8, Appli
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1382	86	4.1	483	4	US-08-842-248A-16	Sequence 16, Appl
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1384	86	4.1	590	4	US-09-499-522A-16	Sequence 16, Appl
1385	86	4.1	630	4	US-10-269-939A-10	Sequence 10, Appl
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1387	86	4.1	1434	1	US-10-080-505-9	Sequence 9, Appli
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1395	85.5	4.1	302	1	US-09-439-999A-6	Sequence 6, Appli
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1411	85.5	4.1	615	4	US-09-949-016-9199	Sequence 9199, Ap
1412	85.5	4.1	615	4	US-08-840-713-35	Sequence 35, Appl
1413	85.5	4.1	617	4	US-08-840-713-37	Sequence 37, Appl
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1418	85.5	4.1	1665	4	US-10-274-978-3	Sequence 3, Appl
1419	85.5	4.1	1665	4	US-10-697-263-2	Sequence 2, Appl
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1424	85	4.1	328	5	PCT-US95-04353-5	Sequence 5, Appl
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1428	85	4.1	1188	1	US-09-201-697-4	Sequence 4, Appl
1429	85	4.1	2032	1	US-09-071-035-458	Sequence 458, Appl
1430	85	4.1	2032	2	US-09-071-035-462	Sequence 462, App
1431	85	4.1	2032	5	US-09-071-035-466	Sequence 466, App
1432	85	4.1	2054	4	US-09-134-000C-6612	Sequence 6612, Ap
1433	85	4.1	2409	6	Patent No. 5180808-2	Patent No. 5180808
1434	85	4.1	2409	6	Patent No. 5180808-2	Patent No. 5180808
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1436	84.5	4.0	119	4	US-10-274-978-31	Sequence 31, Appl
1437	84.5	4.0	119	4	US-10-697-263-31	Sequence 31, Appl
1438	84.5	4.0	241	4	US-08-411-295F-94	Sequence 94, Appl
1439	84.5	4.0	249	2	US-08-797-468-18	Sequence 18, Appl
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1441	84.5	4.0	419	6	US-09-984-186-18	Sequence 18, Appl
1442	84.5	4.0	457	6	US-08-416-478A-8	Sequence 8, Appl
1443	84.5	4.0	457	2	US-08-474-988B-8	Sequence 8, App
1444	84.5	4.0	457	2	US-08-394-442B-8	Sequence 8, Appl
1445	84.5	4.0	524	4	US-09-270-767-44009	Sequence 44009, A
1446	84.5	4.0	650	3	US-09-362-525-2	Sequence 2, Appl
1447	84	4.0	152	2	Patent No. 5169835	Patent No. 5169835
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1449	84	4.0	223	4	US-08-467-602-223	Sequence 223, Appl
1450	84	4.0	230	4	US-08-467-602-223	Sequence 223, App
1451	84	4.0	230	4	US-08-411-295F-149	Sequence 149, App
1452	84	4.0	241	2	US-08-224-591-18	Sequence 18, Appl
1453	84	4.0	241	2	US-08-926-789-18	Sequence 18, Appl
1454	84	4.0	245	3	US-09-069-821-5	Sequence 5, Appl
1455	84	4.0	245	4	US-09-956-086-5	Sequence 5, Appl
1456	84	4.0	245	4	US-09-956-087-5	Sequence 5, Appl
1457	84	4.0	264	4	US-08-467-602-265	Sequence 265, App
1458	84	4.0	264	3	US-08-411-295F-191	Sequence 191, App
1459	84	4.0	265	3	US-09-420-592A-5	Sequence 5, Appl
1460	84	4.0	265	4	US-09-985-442-5	Sequence 5, Appl
1461	84	4.0	265	4	US-09-983-580-5	Sequence 5, Appl
1462	84	4.0	307	2	US-08-332-562A-83	Sequence 83, Appl
1463	84	4.0	315	4	US-09-949-016-7014	Sequence 7014, Ap
1464	84	4.0	323	4	US-08-684-708A-25	Sequence 25, Appl
1465	84	4.0	450	3	US-08-811-682-2	Sequence 2, Appl
1466	84	4.0	530	3	US-08-477-460B-4	Sequence 4, Appl
1467	84	4.0	530	3	US-08-379-516-4	Sequence 4, Appl
1468	84	4.0	530	3	US-09-329-916-4	Sequence 4, Appl
1469	84	4.0	530	3	US-08-485-372A-4	Sequence 4, Appl
1470	84	4.0	530	4	US-09-409-006A-4	Sequence 4, Appl
1471	84	4.0	530	4	US-08-484-681-4	Sequence 4, Appl
1472	84	4.0	530	4	US-09-766-995-4	Sequence 4, Appl
1473	84	4.0	530	5	PCT-US93-07422-4	Sequence 4, Appl
1474	83.5	4.0	100	4	US-09-858-664A-25	Sequence 25, Appl
1475	83.5	4.0	100	4	US-10-274-978-26	Sequence 26, Appl
1476	83.5	4.0	100	4	US-10-697-263-26	Sequence 26, Appl
1477	83.5	4.0	231	1	US-08-168-091A-4	Sequence 4, Appl
1478	83.5	4.0	241	1	US-08-235-838-5	Sequence 5, Appl
1479	83.5	4.0	241	2	US-08-465-473B-5	Sequence 5, Appl
1480	83.5	4.0	288	2	US-08-147-772-2	Sequence 2, Appl
1481	83.5	4.0	288	2	US-08-456-104-6	Sequence 6, Appl
1482	83.5	4.0	288	2	US-08-101-624-23	Sequence 23, Appl
1483	83.5	4.0	288	2	US-08-751-767A-6	Sequence 6, Appl
1484	83.5	4.0	288	2	US-08-153-262-2	Sequence 2, Appl
1485	83.5	4.0	288	3	US-08-280-757B-29	Sequence 29, Appl
1486	83.5	4.0	288	3	US-08-479-744A-29	Sequence 29, Appl
1487	83.5	4.0	288	3	US-08-159-135-2	Sequence 2, Appl
1488	83.5	4.0	288	3	US-08-205-697A-19	Sequence 19, Appl
1489	83.5	4.0	288	3	US-08-702-525-19	Sequence 19, Appl
1490	83.5	4.0	288	3	US-09-450-798-2	Sequence 2, Appl
1491	83.5	4.0	288	3	US-08-403-253A-2	Sequence 2, Appl
1492	83.5	4.0	288	3	US-08-651-200-13	Sequence 13, Appl
1493	83.5	4.0	288	4	US-09-667-135-34	Sequence 34, Appl
1494	83.5	4.0	288	4	US-08-435-816A-2	Sequence 2, Appl
1495	83.5	4.0	288	4	US-09-425-762-29	Sequence 29, Appl
1496	83.5	4.0	288	4	US-09-837-867A-19	Sequence 19, Appl
1497	83.5	4.0	288	4	US-09-910-174B-5	Sequence 5, Appl
1498	83.5	4.0	288	4	US-09-620-461-5	Sequence 5, Appl
1499	83.5	4.0	288	4	US-08-453-386A-2	Sequence 2, Appl
1500	83.5	4.0	288	4	US-09-206-132-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-254-465A-2

; Sequence 2, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/254,465A
; CURRENT FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 2
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-465A-2

Query Match   80.5%; Score 1688; DB 4; Length 321;
Best Local Similarity   100.0%; Pred. No. 2.6e-167;
Matches 321; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy   61 GSDVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GSDVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180

Qy  181 QTNNQEPIKVATLSTLLFRKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 QTNNQEPIKVATLSTLLFRKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVPAIILILISLCCMVVFT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300

Qy  301 MAYIMLCRKTSQQEHVYEAAR 321
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Db  301 MAYIMLCRKTSQQEHVYEAAR 321
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RESULT 2
US-09-953-499-2
; Sequence 2, Application US/09953499
; Patent No. 6838554
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1 (US)
; CURRENT APPLICATION NUMBER: US/09/953,499
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US/09/254,465
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 2
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-953-499-2

Query Match   80.5%; Score 1688; DB 4; Length 321;
Best Local Similarity   100.0%; Pred. No. 2.6e-167;
Matches 321; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGILLGLLLLGHLTVDIYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGILLGLLLLGHLTVDIYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy   61 GSDPVTIFLRDSSGDHIQOAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GSDPVTIFLRDSSGDHIQOAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQQARGSPPISYIWYKQ 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQQARGSPPISYIWYKQ 180

Qy 181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240

Qy 241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300

Qy 301 MAYIMLCRKTSQQEHVYEAAR 321
        ||||||||||||||||||||
Db 301 MAYIMLCRKTSQQEHVYEAAR 321
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RESULT 3
US-09-369-247-63
; Sequence 63, Application US/09369247
; Patent No. 6569992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: Patentin Ver. 2.0
US-09-369-247-63
; SEQ ID NO 63
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (306)
; OTHER INFORMATION: Xaa equals stop translation
US-09-369-247-63

Query Match      73.7%;  Score 1547;  DB 4;  Length 306;
Best Local Similarity   76.2%;  Pred. No. 1.2e-152;
Matches 304;  Conservative   0;  Mismatches   1;  Indels  94;  Gaps   1;

Qy    1 MGILLGLLLLGHLTVDIYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGILLGLLLLGHLTVDIYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60

Qy   61 GSDPVTIFLRDSSGDHIQOAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GSDPVTIFLRDSSGDHIQOAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy  121 DGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQQARGSPPISYIWYKQ 180
        ||||||||||||||||
Db  121 DGNQVVRDKITELRVQ--------------------------- 136

Qy  181 QTNNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
                                              |||||||||||
Db  137 -----------------------------------KHSSKLLKTK 146

Qy  241 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  147 TEAPTTMTYPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFT 206

Qy  301 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  207 MAYIMLCRKTSQQEHVYEAARAHAREANDSGETMRVAIFASGCSSDEPTSQNLGNNYSDE 266

Qy  361 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 399
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Db  267 PCIGQEYQIIAQINGNYARLLDTVPLDYEFLATEGKSVC 305
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RESULT 4
US-09-763-902B-6
; Sequence 6, Application US/09763902B
; Patent No. 6838241
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: YUE, Henry

; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: GORGONE, Gina A.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: PROTEIN TRANSPORT-ASSOCIATED MOLECULES
; FILE REFERENCE: PF-0577 PCT
; CURRENT APPLICATION NUMBER: US/09/763,902B
; CURRENT FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: 60/098,206
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6838241871275CD1
US-09-763-902B-6

Query Match   41.5%; Score 870; DB 4; Length 175;
Best Local Similarity   64.7%; Pred. No. 2.1e-82;
Matches 174; Conservative   0; Mismatches   1; Indels   94; Gaps   1;

Qy   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLLVKMLVQR 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLLVKMLVQR 60

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTP 120

Qy   121 DGNQVVRDKITELRVQKLSVSKEPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQ 180
           ||||||||||||||||
Db   121 DGNQVVRDKITELRVQ 136

Qy   181 QTNQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTK 240
                                                               |||||||||
Db   137 --KHSSKLLKTK 146

Qy   241 TEAPTIMTYPLKATSTVKQSWDWTTDMDG 269
           |||||||||||||||||||||||||||||
Db   147 TEAPTIMTYPLKATSTVKQSWDWTTDMDG 175

RESULT 5
US-09-188-930-189
; Sequence 189, Application US/0918930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 189
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (247)...(247)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (289)...(289)

US-09-188-930-189

Query Match   8.5%; Score 178.5; DB 3; Length 299;
Best Local Similarity   26.5%; Pred. No. 7e-10;
Matches   65; Conservative 36; Mismatches 93; Indels   51; Gaps   11;

Qy   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLLVKMLVQR 60
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Db   17 LAILLCSLALGSVTVHS-SEPEVRIPEN-----NPVKLSCAY---SGFSSPRVEW----- 62

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK-----VPGDVSLQLSTLEMDDRSHYTCEV 115
          : |::   :: : ::   :: : :   :|:|:|:|:||:||||||:||:|:|
Db   63 ------------KFDQGDTTRLVCYNNKIIASYEDRVTFLPTGITFKSVTRB--DIGTYTCMV 111

Qy   116 TWQTPDGNQVVRDKITELRVQKLSVSKEPTVTTGSGYGFTVPQGMRISLQCQAR-GSPPIS 174
          : |:| ||:|:||:|:|:   :|: :: |:::: |: :|:::||::|: : |||: |
Db   112 SEEGGNSYGEVKVLIVL-----VPPSKPTVNIPS---SATIGNRAVITCSEQDGSPFSE 163

Qy   175 YIWYK-----QQTN-------NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH 222
          |:|:| ::| |:| :|| |: :::|:::: :||:|:|:|:| | |: |
Db   164 YTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT 223

Qy   223 SDIVK 227
          |::|:
Db   224 SNAVR 228

RESULT 6
US-09-188-930-331
; Sequence 331, Application US/0918930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 331
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (247)...(247)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (289)...(289)

US-09-188-930-331

Query Match   8.5%; Score 178.5; DB 3; Length 299;
Best Local Similarity   26.5%; Pred. No. 7e-10;
Matches   65; Conservative 36; Mismatches 93; Indels   51; Gaps   11;

Qy   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLLVKMLVQR 60
          : ||| :| ||:|::   ::   : |:   :|:   :|: |:|:
Db   17 LAILLCSLALGSVTVHS-SEPEVRIPEN-----NPVKLSCAY---SGFSSPRVEW----- 62

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK-----VPGDVSLQLSTLEMDDRSHYTCEV 115
          : |::   :: : ::   :: : :   :|:|:|:|:||:||||||:||:|:|
Db   63 ------------KFDQGDTTRLVCYNNKIIASYEDRVTFLPTGITFKSVTRB--DIGTYTCMV 111

Qy   116 TWQTPDGNQVVRDKITELRVQKLSVSKEPTVTTGSGYGFTVPQGMRISLQCQAR-GSPPIS 174
          : |:| ||:|:||:|:|:   :|: :: |:::: |: :|:::||::|: : |||: |
Db   112 SEEGGNSYGEVKVLIVL-----VPPSKPTVNIPS---SATIGNRAVITCSEQDGSPFSE 163

Qy   175 YIWYK-----QQTN-------NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH 222
          |:|:| ::| |:| :|| |: :::|:::: :||:|:|:|:| | |: |
Db   164 YTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT 223

Qy   223 SDIVK 227
          |::|:
Db   224 SNAVR 228

RESULT 7
US-09-462-270-2
; Sequence 2, Application US/09462270
; Patent No. 6358707
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: Human F11 Antigen: A Cell Surface
; TITLE OF INVENTION: Receptor Involved in Platelet Aggregation
; FILE REFERENCE: GH-70150US
; CURRENT APPLICATION NUMBER: US/09/462,270
; CURRENT FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 60/052,186
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 299
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-462-270-2

Query Match   8.5%;   Score 178.5; DB 3; Length 299;
Best Local Similarity   26.5%; Pred. No. 7e-10;
Matches   65; Conservative   36; Mismatches   93; Indels   51; Gaps   11;

Qy   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
            |:||| |||||||:||:| |:||:||: ::| |:| ||:||| |:| |:||:
Db   17 LAILLCSLALGSVTVHS-SEPEVRIPEN------NPVKLSCAY----SGFSSPRVEW---- 62

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK-----VPGDVSLQLSTLEMDDRSHYTCEV 115
            |: || |:| :| :: ||:| |:| :: ||||:| ||::||:| ||:||
Db   63 ------KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTRE--DTGTYTCMV 111

Qy   116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVVTGSSGYGFTVPQGMRISLQCQAR-GSPPIS 174
            || | ||:||||| |:|||| :| |: | :|:| || | |:||:|:| |||||
Db   112 SEEGGNSYGEVKVKLIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSE 163

Qy   175 YIWYK----QQTN------NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH 222
            |:|:| ||:| |:| | | |:| :|: :|::||:| | :| |:|
Db   164 YTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT 223

Qy   223 SDIVK 227
            |:||:
Db   224 SNAVR 228

RESULT 8
US-09-254-465A-1
; Sequence 1, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; TITLE OF INVENTION: OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1212R1 (US)
; CURRENT APPLICATION NUMBER: US/09/254,465A
; CURRENT FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437

; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 1
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-465A-1

Query Match   8.5%;   Score 178.5; DB 4; Length 299;
Best Local Similarity   26.5%; Pred. No. 7e-10;
Matches   65; Conservative   36; Mismatches   93; Indels   51; Gaps   11;

Qy   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
            |:||| |||||||:||:| |:||:||: ::| |:| ||:||| |:| |:||:
Db   17 LAILLCSLALGSVTVHS-SEPEVRIPEN------NPVKLSCAY----SGFSSPRVEW---- 62

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK-----VPGDVSLQLSTLEMDDRSHYTCEV 115
            |: || |:| :| :: ||:| |:| :: ||||:| ||::||:| ||:||
Db   63 ------KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTRE--DTGTYTCMV 111

Qy   116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVVTGSSGYGFTVPQGMRISLQCQAR-GSPPIS 174
            || | ||:||||| |:|||| :| |: | :|:| || | |:||:|:| |||||
Db   112 SEEGGNSYGEVKVKLIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSE 163

Qy   175 YIWYK----QQTN------NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH 222
            |:|:| ||:| |:| | | |:| :|: :|::||:| | :| |:|
Db   164 YTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT 223

Qy   223 SDIVK 227
            |:||:
Db   224 SNAVR 228

RESULT 9
US-09-312-283C-189
; Sequence 189, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011C2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-189

Query Match   8.5%;   Score 178.5; DB 4; Length 299;
Best Local Similarity   26.5%; Pred. No. 7e-10;
Matches   65; Conservative   36; Mismatches   93; Indels   51; Gaps   11;

Qy   1 MGILLGLLLLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
            |:||| |||||||:||:| |:||:||: ::| |:| ||:||| |:| |:||:
Db   17 LAILLCSLALGSVTVHS-SEPEVRIPEN------NPVKLSCAY----SGFSSPRVEW---- 62

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK-----VPGDVSLQLSTLEMDDRSHYTCEV 115
            |: || |:| :| :: ||:| |:| :: ||||:| ||::||:| ||:||
Db   63 ------KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTRE--DTGTYTCMV 111

Qy   116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVVTGSSGYGFTVPQGMRISLQCQAR-GSPPIS 174
            || | ||:||||| |:|||| :| |: | :|:| || | |:||:|:| |||||
Db   112 SEEGGNSYGEVKVKLIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSE 163

RESULT 10
US-09-312-283C-331
Sequence 331, Application US/09312283C
Patent No. 6573095
GENERAL INFORMATION:

; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.101iC2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 331
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-331

Query Match   8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity   26.5%; Pred. No. 7e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

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Qy    1    MGILLGLILLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR   60
           |||| |||| || || |||| | || ||||
Db    17   LAILLCSLALGSVTVHS-SEPEVRIPEN------NPVKLSCAY---SGFSSPRVEW----   62

Qy    61   GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK-----VPGDVSLQLSTLEMDDRSHYTCEV  115
           ||  |:                              |:  |:
Db    63   ------KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTRE--DTGTYTCMV  111

Qy    116  TWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQAR-GSPPIS  174
           |:|                |:| |
Db    112  SEEGGNSYGEVKVKLIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPSE  163

Qy    175  YIWYK----QQTN-------NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSSEQH  222
           |||                |||
Db    164  YTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT  223

Qy    223  SDIVK  227
           |:|:
Db    224  SNAVR  228
```

; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28311
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
;
; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-119

Query Match   8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity   26.5%; Pred. No. 7e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

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Qy    1    MGILLGLILLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR   60
           |||| |||| || || |||| | || ||||
Db    17   LAILLCSLALGSVTVHS-SEPEVRIPEN------NPVKLSCAY---SGFSSPRVEW----   62

Qy    61   GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK-----VPGDVSLQLSTLEMDDRSHYTCEV  115
           ||  |:                              |:  |:
Db    63   ------KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTRE--DTGTYTCMV  111
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RESULT 11
US-09-907-794A-119
Sequence 119, Application US/0907794A
Patent No. 6653468
GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

RESULT 12

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Qy  116  TWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGPFTVPQGMRISLQCQAR-GSPPIS  174
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Db  112  SEEGGNSYGEVKVKLIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSE  163

Qy  175  YIWYK----QQTN-----NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH  222
              |:|:|          :||            ||||||         :||
Db  164  YTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT  223

Qy  223  SDIVK  227
              |:|:
Db  224  SNAVR  228
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US-09-905-125A-119
; Sequence 119, Application US/0990525A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-119

Query Match   8.5%;   Score 178.5;   DB 4;   Length 299;
Best Local Similarity 26.5%;   Pred. No. 7e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

RESULT 13

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Qy    1  MGILILGLILLIGHLTVDTYGRPILEVPESVTGFWRKGDVNLPCTYDPLQGYTQVLVKWLVQR  60
             :                 |:              :  |:|:
Db   17  LAILLCSLALGSVTVHS-SEPEVRIPEN-----NPVKLSCAY---SGFSSPRVEW----  62

Qy   61  GSDPVTIPLRDSSGDHIQQAKYQGRLHVSHK------VPGDVSLQLSTLEMDDRSHYTCEV  115
             :||         ::     |                    ::       |   |
Db   63  ------KFDQGDTRLVCVNNKITASYEDRVTFLPTGIITPFKSVTRB--DTGTYTCMV  111

Qy  116  TWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGPFTVPQGMRISLQCQAR-GSPPIS  174
             :|:|:|||||  ||||||     |||||
Db  112  SEEGGNSYGEVKVKLIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSE  163

Qy  175  YIWYK----QQTN-----NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH  222
             |:|:|          :||            ||||||         :||
Db  164  YTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT  223

Qy  223  SDIVK  227
             |:|:
Db  224  SNAVR  228
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US-09-902-775A-119
; Sequence 119, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-902-775A-119

Query Match   Best Local Similarity   26.5%;   Score 178.5; DB 4; Length 299;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

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Qy    1 MGILILGLILLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
         ||||| |||| ||| ||:||:  |:|:|:|:||||:|:||:|  |:|:|  |:|
Db   17 LAILLCSLALGSVTVHS-SEPEVRIPEN-----NPVKLSCAY---SGFSSPRVEW----- 62

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK-----VPGDVSLQLSTLEMDDRSHYTCEV 115
         |:|    ::|: |:   :|: :|:          |:| |:|| ||||:||||| ||||
Db   63 -----------KFDQGDTTRLVCYNNKITASYEDRVTFLPTGIFFKSVTRE--DTGTYTCMV 111

Qy  116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSSYGFTVPQGMRISLQCQAR-GSPPIS 174
         :|:: ||  | |:|||||::|    ||||||| |||||  |:||| |||||| |||||
Db  112 SEEGGNSYGEVKVKLIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSE 163

Qy  175 YIWYK----QQTN-------NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH 222
         | |:|    |||:       |:|:|   |:||:|:|:  :||||||| |||:|||||||
Db  164 YTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT 223

Qy  223 SDIVK 227
         |:|:|
Db  224 SNAVR 228
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RESULT 14
US-09-397-243D-3
; Sequence 3, Application US/09972243D
; Patent No. 6659688

; GENERAL INFORMATION:
; APPLICANT: Kornecki, Elizabeth
; APPLICANT: Sobocka, Malgorzata B.
; TITLE OF INVENTION: Human Platelet F11 Receptor
; FILE REFERENCE: 011.00221
; CURRENT APPLICATION NUMBER: US/09/397,243D
; CURRENT FILING DATE: 1999-09-16
; PRIOR APPLICATION NUMBER: 60/100,638
; PRIOR FILING DATE: 1998-09-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-397-243D-3

Query Match   Best Local Similarity   26.5%;   Score 178.5; DB 4; Length 299;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

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Qy    1 MGILILGLILLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
         ||||| |||| ||| ||:||:  |:|:|:|:||||:|:||:|  |:|:|  |:|
Db   17 LAILLCSLALGSVTVHS-SEPEVRIPEN-----NPVKLSCAY---SGFSSPRVEW----- 62

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK-----VPGDVSLQLSTLEMDDRSHYTCEV 115
         |:|    ::|: |:   :|: :|:          |:| |:|| ||||:||||| ||||
Db   63 -----------KFDQGDTTRLVCYNNKITASYEDRVTFLPTGIFFKSVTRE--DTGTYTCMV 111

Qy  116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSSYGFTVPQGMRISLQCQAR-GSPPIS 174
         :|:: ||  | |:|||||::|    ||||||| |||||  |:||| |||||| |||||
Db  112 SEEGGNSYGEVKVKLIVL----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSE 163

Qy  175 YIWYK----QQTN-------NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQH 222
         | |:|    |||:       |:|:|   |:||:|:|:  :||||||| |||:|||||||
Db  164 YTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT 223

Qy  223 SDIVK 227
         |:|:|
Db  224 SNAVR 228
```

RESULT 15
US-09-906-700-119
; Sequence 119, Application US/09906700
; Patent No. 6725535

; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,700
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
;
; SEQ ID NO 119
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-700-119

Query Match   8.5%; Score 178.5; DB 4; Length 299;
Best Local Similarity 26.5%; Pred. No. 7e-10;
Matches 65; Conservative 36; Mismatches 93; Indels 51; Gaps 11;

Qy   1 MGILLGLILLGHLTVDTYGRPILEVPESVTGPWKGDVNLPCTYDPLQGYTQVLVKWLVQR 60
            ||||||||||||||:||||:|:| : |: |: |:|:|: |:|:||
Db   17 LAILLCSLALGSVTVHS-SEPEVRIPEN-------NPVKLSCAY---SGFSSPRVEW---- 62

Qy   61 GSDPVTIFLRDSSGDHIQQAKYQGRLHVSHK------VPGDVSLQLSTLEMDDRSHYTCEV 115
            :   :: |:   : |: || |: ||: || |:
Db   63 --------------KFDQGDTTRLVCVNNKITASYEDRVTFLPTGITFKSVTRE--DTGTYTCMV 111

Qy   116 TWQTPDGNQVVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQAR-GSPPIS 174
            :|||:| : :|| ||: :: :|:|| :   :   :||:| :||||: |:||||
Db   112 SEEGGNSYGEVKVKLIVL-----VPPSKPTVNIPS----SATIGNRAVLTCSEQDGSPPSE 163

Qy   175 YIWYK-----QQTN-------NQEPIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSSEQH 222
            ||:| :| :::| :|||:|||:|:|:|||:||:|: |: :|
Db   164 YTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMT 223

Qy   223 SDIVK 227
            ||:|
Db   224 SNAVR 228

Search completed: March 2, 2005, 15:20:44
Job time : 35 secs

OM protein - protein search, using sw model
Run on: March 2, 2005, 15:22:02 ; Search time 174 seconds
                                     (without alignments)
                                     886.882 Million cell updates/sec

Title: US-10-633-008-32
Perfect score: 2098
Sequence: 1 MGILLGLLLGHLTVDTYGR..........LLDTVPLDYEFLATEGKSVC 399
Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched: 2105692 seqs, 38760381 residues
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%

Database :   A_Geneseq_16Dec04:*
                Listing first 1500 summaries
                1: geneseqp1980s:*
                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s: ,
                6: geneseqp2003aa:*
                7: geneseqp2003ba:*
                8: geneseqp2008s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                              SUMMARIES
No.   Score   Match Length DB ID   Description

RESULT 1
ID   AAB19396 standard; protein; 399 AA.
DE   Amino acid sequence of a human secreted protein.
PN   WO2006175S:A2.
PD   19-OCT-2000.
PA   (CHIR-)=CHIRON CORP.
        Query Match   100.0%;   Score 2098; DB 3;   Length 399;
        Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 2
ID   AAE04230 standard; protein; 399 AA.
DE   Human gene 11 encoded secreted protein HMSOW51, SEQ ID NO:85.
PN   WO200136432-A2.
PD   25-MAY-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
        Query Match   100.0%;   Score 2098; DB 3;   Length 399;
        Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 3
ID   AAE04208 standard; protein; 399 AA.
DE   Human gene 11 encoded secreted protein HMSOW51, SEQ ID NO:63.
PN   WO200136432-A2.
PD   25-MAY-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
        Query Match   100.0%;   Score 2098; DB 4;   Length 399;
        Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 4
ID   ABG64488 standard; protein; 399 AA.
DE   Human albumin fusion protein #1163.
PN   WO200177137-A1.
PD   18-OCT-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
        Query Match   100.0%;   Score 2098; DB 5;   Length 399;
        Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 5
ID   ABG64487 standard; protein; 399 AA.
DE   Human albumin fusion protein #1162.
PN   WO200177137-A1.
PD   18-OCT-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
        Query Match   100.0%;   Score 2098; DB 5;   Length 399;
        Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 6
ID   ABU03567 standard; protein; 399 AA.

SEQ ID NO. 8

DE   Angiogenesis-associated human protein sequence #112.
PN   WO200279492-A2.
PD   10-OCT-2002.
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
        Query Match   100.0%;   Score 2098; DB 6;   Length 399;
        Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 7
ID   ADA57183 standard; protein; 399 AA.
DE   Human secreted protein #466.
PN   WO2002102994-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
        Query Match   100.0%;   Score 2098; DB 6;   Length 399;
        Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 8
ID   ADA41052 standard; protein; 399 AA.
DE   Human secreted protein.
PN   WO2002102993-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
        Query Match   100.0%;   Score 2098; DB 6;   Length 399;
        Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 9
ID   ABR47904 standard; protein; 399 AA.
DE   Human secreted protein, SEQ ID 795.
PN   WO200295010-A2.
PD   28-NOV-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
        Query Match   100.0%;   Score 2098; DB 7;   Length 399;
        Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 10
ID   ABR00157 standard; protein; 399 AA.
DE   Human gene 147 encoded secreted protein HSDBK49, SEQ ID NO:446.
PN   WO200276488-A1.
PD   03-OCT-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
        Query Match   100.0%;   Score 2098; DB 6;   Length 399;
        Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 11
ID   ADB91646 standard; protein; 399 AA.
DE   Human secreted protein #SEQ ID 592.
PN   WO200304622-A2.
PD   16-JAN-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
        Query Match   100.0%;   Score 2098; DB 7;   Length 399;
        Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 12
ID   ADC74298 standard; protein; 399 AA.
DE   Human secreted protein - SEQ ID 931.
PN   WO200303063-A2.
PD   08-MAY-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
        Query Match   100.0%;   Score 2098; DB 7;   Length 399;
        Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 13
ID   ADL77755 standard; protein; 399 AA.
DE   Albumin fusion protein related therapeutic protein X, SEQ ID No 1237.
PN   US20040101034-A1.
PD   15-JAN-2004.
PA   (ROSE/) ROSEN C A.
        (HASE/) HASELTINE W A.
        Query Match   100.0%;   Score 2098; DB 8;   Length 399;
        Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 14
ID   ADL77754 standard; protein; 399 AA.
DE   Albumin fusion protein related therapeutic protein X, SEQ ID No 1236.
PN   US20040101034-A1.
PD   15-JAN-2004.
PA   (ROSE/) ROSEN C A.
        (HASE/) HASELTINE W A.
        Query Match   100.0%;   Score 2098; DB 8;   Length 399;
        Best Local Similarity 100.0%; Pred. No. 2.2e-172;
RESULT 15

ID ADL67172 standard; protein; 399 AA.
DE Human B7-H6 protein SEQ ID NO:42.
PN WO200402259A-A2.
PD 18-MAR-2004.
PA (CYTO-) CYTOS BIOTECHNOLOGY AG
Query Match 100.0%; Score 2098; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.2e-172;

RESULT 16
ID ADN35311 standard; protein; 399 AA.
DE Human STIgMA protein.
PN WO200403105-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2098; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.2e-172;

RESULT 17
ID ABMB2416 standard; protein; 399 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO34043, SEQ:6205.
PN WO200404170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2098; DB 8; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.2e-172;

RESULT 18
ID ADP23762 standard; protein; 399 AA.
DE PRO polypeptide, SEQ ID NO: 3986.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 99.4%; Score 2085; DB 4; Length 399;
Best Local Similarity 99.2%; Pred. No. 2.9e-171;

RESULT 19
ID AAM93874 standard; protein; 399 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3986.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 99.4%; Score 2085; DB 8; Length 399;
Best Local Similarity 99.2%; Pred. No. 2.9e-171;

RESULT 20
ID ADL31953 standard; protein; 386 AA.
DE Human gene 11 encoded secreted protein fragment, SEQ ID NO:154.
PN WO200136432-A2.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 97.0%; Score 2035; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 5.8e-167;

RESULT 21
ID AAB04290 standard; protein; 386 AA.
DE Amino acid sequence of the PRO362 polypeptide.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 99.2%; Score 2085; DB 8; Length 399;
Best Local Similarity 99.4%; Pred. No. 2.9e-171;

RESULT 22
ID AAY23322 standard; protein; 321 AA.
DE Human PRO 362 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;

RESULT 23
ID AAY41691 standard; protein; 321 AA.
DE Human PRO 362 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;

RESULT 24
ID AAB33429 standard; protein; 321 AA.
DE Human PRO362 protein UNQ317 SEQ ID NO:80.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;

RESULT 25
ID AAB44247 standard; protein; 321 AA.
DE Human PRO362 (UNQ317) protein sequence SEQ ID NO:52.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;

RESULT 26
ID AAY95346 standard; protein; 321 AA.
DE Human PRO362 antitumour protein.
PN WO200037638-A2.
PD 29-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;

RESULT 27
ID AAB24047 standard; protein; 321 AA.
DE Human PRO362 protein sequence SEQ ID NO:14.
PN WO200053754-A1.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;

RESULT 28
ID ABO25193 standard; protein; 321 AA.
DE Novel human secreted and transmembrane protein PRO362.
PN US200305023-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;

RESULT 29
ID ABO72199 standard; protein; 321 AA.
DE Novel human secreted and transmembrane protein PRO362.
PN US200219270G-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;

RESULT 30
ID ABU84879 standard; protein; 321 AA.
DE Human secreted and transmembrane polypeptide PRO362.
PN US200217755-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;

RESULT 31
ID ABU61077 standard; protein; 321 AA.
DE Human PRO362 polypeptide.
PN US200216928-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;

RESULT 32
ID ABU80346 standard; protein; 321 AA.
DE Human secreted/transmembrane protein PRO362.
PN US200304102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 80.5%; Score 1688; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;

RESULT 33
ID ABU07737 standard; protein; 321 AA.
DE Human A-33 related antigen PRO362.

PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 6; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 34
ID ADA24591 standard; protein; 321 AA.
DE Novel human secreted and transmembrane protein PRO362.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 6; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 35
ID ABO19648 standard; protein; 321 AA.
DE Novel human secreted and transmembrane protein PRO362.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 6; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 36
ID ADA12252 standard; protein; 321 AA.
DE Human secreted/transmembrane protein; 321 AA.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 6; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 37
ID ABO19539 standard; protein; 321 AA.
DE Novel human secreted and transmembrane polypeptide PRO362.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 6; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 38
ID ADB73558 standard; protein; 321 AA.
DE Human PRO polypeptide #7.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 6; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 39
ID ADB76274 standard; protein; 321 AA.
DE Human PRO polypeptide #7.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 7; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 40
ID ADC43700 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 7; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 41
ID ADC61460 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 7; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 42
ID ADC63424 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003054405-A1.
PD 20-MAR-2003.

PA (GETH') GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 7; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 43
ID ADC66524 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 7; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 44
ID ADC68648 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 7; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 45
ID ADC62708 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 7; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 46
ID ADC67773 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 7; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 47
ID ADC41093 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 7; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 48
ID ADC67148 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003073113-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 7; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 49
ID ADC62084 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 7; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 50
ID ADC41717 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
    Query Match   80.5%;   Score 1688; DB 7; Length 321;
    Best Local Similarity 100.0%;   Pred. No. 4.3e-137;

RESULT 51
ID ADC78883 standard; protein; 321 AA.
DE Human PRO protein #56.
PN W02003034984-A2.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match   80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 52
ID ADE49086 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US20030967744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match   80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 53
ID ADE35140 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US20030203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match   80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 54
ID ADE16254 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US20030203435-A1.
PD 30-OCT-2003
PA (GETH) GENENTECH INC.
Query Match   80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 55
ID ADD72069 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US20030203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match   80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 56
ID ADD72227 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US20031947781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match   80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 57
ID ADE16878 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US20030203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match   80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 58
ID ADF46892 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US20030195533-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match   80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 59
ID ADG52649 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US20030216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match   80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 60
ID ADG59969 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US20030206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match   80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;

Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 61
ID ADH62529 standard; protein; 321 AA.
DE Human PRO362 protein encoded by DNA45416.
PN US20031715568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
Query Match   80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 62
ID ADI60729 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US20030777700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   80.5%; Score 1688; DB 7; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 63
ID ADE48386 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US20030104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match   80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 64
ID ADE89487 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US20031130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match   80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
RESULT 65
ID ADF61127 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US20030195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match   80.5%; Score 1688; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;

RESULT 66
ID ADF39819 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 67
ID ADF45615 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 68
ID ADF24011 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 69
ID ADF40443 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 70
ID ADF23387 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 71
ID ADF33370 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 72
ID ADF26837 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 73
ID ADF27473 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 74
ID ADF41067 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 75

RESULT 76
ID ADF32746 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 77
ID ADF25112 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 78
ID ADF26213 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 79
ID ADF34002 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 80
ID ADF46239 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 81
ID ADG50225 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 82
ID ADG49601 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 83
ID ADG51473 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 84
ID ADG48977 standard; protein; 321 AA.
DE Human secreted/transmembrane protein, PRO362.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1688; DB 8; Length 321;
Best Local Similarity 80.5%; Pred. No. 4.3e-137;

RESULT 84
ID ADG48353 standard; protein; 321 AA.

DE   Human secreted/transmembrane protein, PRO362.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
RESULT 85
Best Local Similarity   80.5%;
Query Match   100.0%;   Score 1688;   DB 8;   Length 321;
Pred. No. 4.3e-137;
ID   ADG50849 standard; protein; 321 AA.
DE   Human secreted/transmembrane protein, PRO362.
PN   US20040005312-A1.
PD   08-JAN-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1688;   DB 8;   Length 321;
Pred. No. 4.3e-137;
RESULT 86
Best Local Similarity   80.5%;
ID   ADG58793 standard; protein; 321 AA.
DE   Human secreted/transmembrane protein, PRO362.
PN   US20040005657-A1.
PD   08-JAN-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1688;   DB 8;   Length 321;
Pred. No. 4.3e-137;
RESULT 87
Best Local Similarity   80.5%;
ID   ADG62249 standard; protein; 321 AA.
DE   Human secreted/transmembrane protein, PRO362.
PN   US20040006219-A1.
PD   08-JAN-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1688;   DB 8;   Length 321;
Pred. No. 4.3e-137;
RESULT 88
Best Local Similarity   80.5%;
ID   ADH25274 standard; protein; 321 AA.
DE   Human neurotrimin homologue related protein sequence SEQ ID NO:52.
PN   EP1386931-A1.
PD   04-FEB-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1688;   DB 8;   Length 321;
Pred. No. 4.3e-137;
RESULT 89
Best Local Similarity   80.5%;
ID   ADM17051 standard; protein; 321 AA.
DE   Human secreted/transmembrane protein, PRO362.
PN   US20040048332-A1.
PD   11-MAR-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1688;   DB 8;   Length 321;
Pred. No. 4.3e-137;
RESULT 90
Best Local Similarity   80.5%;
ID   ADL06885 standard; protein; 321 AA.
DE   Human secreted/transmembrane protein, PRO362.
PN   US20040063921-A1.
PD   01-APR-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1688;   DB 8;   Length 321;
Pred. No. 4.3e-137;
RESULT 91
Best Local Similarity   80.5%;
ID   ADN35285 standard; protein; 321 AA.
DE   Human STIGMA protein.
PN   WO2004031105-A2.
PD   15-APR-2004.
PA   (GETH) GENENTECH INC.
Query Match   100.0%;   Score 1688;   DB 8;   Length 321;
Pred. No. 4.3e-137;
RESULT 92
Best Local Similarity   80.5%;
ID   ADA57531 standard; protein; 305 AA.
DE   Human secreted protein #466.
PN   WO2002102994-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   73.7%;   Score 1547;   DB 6;   Length 305;
Pred. No. 6.1e-125;
RESULT 93
Best Local Similarity   76.2%;
ID   ADA41415 standard; protein; 305 AA.
DE   Human secreted protein.

PN   WO2002102993-A2.
PD   27-DEC-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   73.7%;   Score 1547;   DB 6;   Length 305;
Pred. No. 6.1e-125;
RESULT 94
Best Local Similarity   76.2%;
ID   APR48114 standard; protein; 305 AA.
DE   Human secreted protein, SEQ ID 1005.
PN   WO200295010-A2.
PD   28-NOV-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   73.7%;   Score 1547;   DB 6;   Length 305;
Pred. No. 6.1e-125;
RESULT 95
Best Local Similarity   76.2%;
ID   ABR00282 standard; protein; 305 AA.
DE   Human gene 147 encoded secreted protein HSDEK49, SEQ ID NO:571.
PN   WO200276488-A1.
PD   03-OCT-2002.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   73.7%;   Score 1547;   DB 6;   Length 305;
Pred. No. 6.1e-125;
RESULT 96
Best Local Similarity   76.2%;
ID   ADB91804 standard; protein; 305 AA.
DE   Human secreted protein #SEQ ID 750.
PN   WO2003004622-A2.
PD   16-JAN-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   73.7%;   Score 1547;   DB 7;   Length 305;
Pred. No. 6.1e-125;
RESULT 97
Best Local Similarity   76.2%;
ID   ADC74547 standard; protein; 305 AA.
DE   Human secreted protein - SEQ ID 1180.
PN   WO2003038063-A2.
PD   08-MAY-2003.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   73.7%;   Score 1547;   DB 7;   Length 305;
Pred. No. 6.1e-125;
RESULT 98
Best Local Similarity   76.2%;
ID   ADN35312 standard; protein; 305 AA.
DE   Human short STIGMA protein.
PN   WO2004031105-A2.
PD   15-APR-2004.
PA   (GETH) GENENTECH INC.
Query Match   73.7%;   Score 1547;   DB 8;   Length 305;
Pred. No. 6.1e-125;
RESULT 99
Best Local Similarity   76.2%;
ID   AAY30814 standard; protein; 306 AA.
DE   Human secreted protein encoded from gene 4.
PN   WO9940100-A1.
PD   12-AUG-1999.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   73.7%;   Score 1547;   DB 2;   Length 306;
Pred. No. 6.2e-125;
RESULT 100
Best Local Similarity   76.2%;
ID   ADL67174 standard; protein; 281 AA.
DE   Human B7-H6(ECD) protein SEQ ID NO:44.
PN   WO2004002594-A2.
PD   18-MAR-2004.
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match   70.5%;   Score 1480;   DB 8;   Length 281;
Pred. No. 6.1e-125;
RESULT 101
Best Local Similarity   46.9%;
ID   AAM93588 standard; protein; 184 AA.
DE   Human polypeptide, SEQ ID NO: 3387.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
Query Match   100.0%;   Score 983;   DB 4;   Length 184;
Pred. No. 3.4e-119;
RESULT 102
Best Local Similarity   100.0%;
ID   ADL31354 standard; protein; 184 AA.
DE   Human protein encoded by a full length cDNA clone SeqID 3387.
PN   EP1396543-A2.
Pred. No. 1.6e-76;

```
PD   10-MAR-2004!
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match       46.9%;  Score 983;  DB 8;  Length 184;
Best Local Similarity  100.0%;  Pred. No. 1.6e-76;

RESULT 103
ID   AAY82322 standard; protein; 175 AA.
DE   Human protein transport molecule (PTAM) SEQ ID NO:6.
PN   WO20001270703-A2.
PD   09-MAR-2000.
PA   (INCY-) INCYTE PHARM INC.
Query Match       41.5%;  Score 870;  DB 3;  Length 175;
Best Local Similarity   64.7%;  Pred. No. 8.8e-67;

RESULT 104
ID   ADK70486 standard; protein; 175 AA.
DE   Respiratory disease differentially expressed protein #52.
PN   WO2003101283-A2.
PD   11-DEC-2003.
PA   (INCY-) INCYTE CORP.
Query Match       41.5%;  Score 870;  DB 3;  Length 175;
Best Local Similarity   64.7%;  Pred. No. 8.8e-67;

RESULT 105
ID   ADL67144 standard; protein; 280 AA.
DE   Mouse B7-H6 protein SEQ ID NO:14.
PN   WO2004022594-A2.
PD   18-MAR-2004.
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match       40.0%;  Score 840;  DB 8;  Length 280;
Best Local Similarity   47.4%;  Pred. No. 6.8e-64;

RESULT 106
ID   ADN35313 standard; protein; 280 AA.
DE   Murine STIGMA protein.
PN   WO2004031105-A2.
PD   15-APR-2004.
PA   (GETH ) GENENTECH INC.
Query Match       40.0%;  Score 840;  DB 8;  Length 280;
Best Local Similarity   47.4%;  Pred. No. 6.8e-64;

RESULT 107
ID   ADL67146 standard; protein; 188 AA.
DE   Mouse B7-H6(BCD) protein SEQ ID NO:16.
PN   WO2004022594-A2.
PD   18-MAR-2004.
PA   (CYTO-) CYTOS BIOTECHNOLOGY AG.
Query Match       29.2%;  Score 613;  DB 8;  Length 188;
Best Local Similarity   45.7%;  Pred. No. 1.6e-44;

RESULT 108
ID   AAE10596 standard; protein; 93 AA.
DE   Human macrophage-expressed protein #21.
PN   WO200164839-A2.
PD   07-SEP-2001.
PA   (HYSE-) HYSEQ INC.
Query Match       23.5%;  Score 492;  DB 4;  Length 93;
Best Local Similarity   98.9%;  Pred. No. 1.7e-34;

RESULT 109
ID   ADH80723 standard; protein; 300 AA.
DE   Human polypeptide #10.
PN   US2003232054-A1.
PD   18-DEC-2003.
PA   (TANG/) TANG Y T.
PA   (LIUC/) LIU C.
PA   (ASUN/) ASUNDI V.
PA   (CHEN/) CHEN R.
PA   (QIAN/) QIAN X B.
PA   (WANG/) WANG Z W.
PA   (WEHR/) WEHRMAN T.
PA   (ZHAN/) ZHANG J.
PA   (ZHOU/) ZHOU P.
PA   (CAOY/) CAO Y.
PA   (DRMA/) DRMANAC R T.
Query Match       8.6%;  Score 180;  DB 8;  Length 300;
Best Local Similarity   27.9%;  Pred. No. 8.1e-07;

RESULT 110
ID   AAY23321 standard; protein; 299 AA.
DE   Amino acid sequence of the PRO301 polypeptide.
PN   WO9927098-A2.
PD   03-JUN-1999.
PA   (GETH ) GENENTECH INC.
Query Match       8.5%;  Score 178.5;  DB 2;  Length 299;
Best Local Similarity   26.5%;  Pred. No. 1.1e-06;

RESULT 111
ID   AAW74464 standard; protein; 299 AA.
DE   F11 antigen protein sequence.
PN   WO9902561-A1.
PD   21-JAN-1999.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
Query Match       8.5%;  Score 178.5;  DB 2;  Length 299;
Best Local Similarity   26.5%;  Pred. No. 1.1e-06;

RESULT 112
ID   AAY08071 standard; protein; 299 AA.
DE   Human PRO307 protein.
PN   WO9914241-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.
Query Match       8.5%;  Score 178.5;  DB 2;  Length 299;
Best Local Similarity   26.5%;  Pred. No. 1.1e-06;

RESULT 113
ID   AAY13364 standard; protein; 299 AA.
DE   Human A33 receptor homologue, SEQ ID NO:331.
PN   WO9914328-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.
Query Match       8.5%;  Score 178.5;  DB 2;  Length 299;
Best Local Similarity   26.5%;  Pred. No. 1.1e-06;

RESULT 114
ID   AAY76011 standard; protein; 299 AA.
DE   Amino acid sequence of protein PRO301.
PN   WO9955865-A1.
PD   04-NOV-1999.
PA   (GENE-) GENESIS RES & DEV CORP LTD.
Query Match       8.5%;  Score 178.5;  DB 3;  Length 299;
Best Local Similarity   26.5%;  Pred. No. 1.1e-06;

RESULT 115
ID   AAY76076 standard; protein; 299 AA.
DE   Human A33 receptor homologue, SEQ ID NO:189.
PN   WO9955865-A1.
PD   04-NOV-1999.
PA   (GENE-) GENESIS RES & DEV CORP LTD.
Query Match       8.5%;  Score 178.5;  DB 3;  Length 299;
Best Local Similarity   26.5%;  Pred. No. 1.1e-06;

RESULT 116
ID   AAY70670 standard; protein; 299 AA.
DE   Human A33 receptor protein.
PN   WO200015797-A2.
PD   23-MAR-2000.
PA   (GETH ) GENENTECH INC.
Query Match       8.5%;  Score 178.5;  DB 3;  Length 299;
Best Local Similarity   26.5%;  Pred. No. 1.1e-06;

RESULT 117
ID   AAB24405 standard; protein; 299 AA.
DE   Human PRO301 protein sequence SEQ ID NO:90.
PN   WO2000032221-A2.
PD   08-JUN-2000.
PA   (GETH ) GENENTECH INC.
Query Match       8.5%;  Score 178.5;  DB 3;  Length 299;
Best Local Similarity   26.5%;  Pred. No. 1.1e-06;

RESULT 118
ID   AAY95344 standard; protein; 299 AA.
DE   Human PRO301 antitumour protein.
PN   WO2000037638-A2.
PD   29-JUN-2000.
PA   (GETH ) GENENTECH INC.
Query Match       8.5%;  Score 178.5;  DB 3;  Length 299;
Best Local Similarity   26.5%;  Pred. No. 1.1e-06;

RESULT 119
ID   AAB80232 standard; protein; 299 AA.
DE   Human PRO301 protein.
PN   WO20001043 11-A1.
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PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
RESULT 120
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 4; Length 299;
ID AAM93577 standard; protein; 299 AA.
DE Human polypeptide, SEQ ID NO: 3365.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
RESULT 121
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 4; Length 299;
ID AAB56015 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 331.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
RESULT 122
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 4; Length 299;
ID AAB55950 standard; protein; 299 AA.
DE Skin cell protein, SEQ ID NO: 189.
PN WO200069884-A2.
PD 23-NOV-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
RESULT 123
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 4; Length 299;
ID AAB31202 standard; protein; 299 AA.
DE Amino acid sequence of human polypeptide PRO301.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
RESULT 124
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 4; Length 299;
ID AAU00823 standard; protein; 299 AA.
DE Human immune response protein PRO301 (UNQ264).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
RESULT 125
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 4; Length 299;
ID AAU12354 standard; protein; 299 AA.
DE Human PRO301 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
RESULT 126
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 4; Length 299;
ID AAB53086 standard; protein; 299 AA.
DE Human angiogenesis-associated protein PRO301, SEQ ID NO:119.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
RESULT 127
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 4; Length 299;
ID AAU14405 standard; protein; 299 AA.
DE Human novel protein #276.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
RESULT 128
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 4; Length 299;
ID AAU14404 standard; protein; 299 AA.
DE Human novel protein #275.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
RESULT 129
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 4; Length 299;
ID AAU14168 standard; protein; 299 AA.
DE Human novel protein #39.
PN WO200155437-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
RESULT 130
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 4; Length 299;
ID AAE03840 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein fragment, SEQ ID NO:148.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
RESULT 131
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 4; Length 299;
ID AAE03896 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein HACAA29, SEQ ID NO: 86.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
RESULT 132
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 4; Length 299;
ID AAE03870 standard; protein; 299 AA.
DE Human gene 23 encoded secreted protein HACAA29, SEQ ID NO:116.
PN WO200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
RESULT 133
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 4; Length 299;
ID AAB90290 standard; protein; 299 AA.
DE Human polypeptide SEQ ID NO 2666.
PN WO200190304-A1.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
RESULT 134
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 4; Length 299;
ID ABB84843 standard; protein; 299 AA.
DE Human PRO301 protein sequence SEQ ID NO:54.
PN WO200206690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
RESULT 135
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 5; Length 299;
ID ABG64551 standard; protein; 299 AA.
DE Human albumin fusion protein #1226.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
RESULT 136
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 5; Length 299;
ID ABG64552 standard; protein; 299 AA.
DE Human albumin fusion protein #1227.
PN WO200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
RESULT 137
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 5; Length 299;
ID ABB72215 standard; protein isolated from skin cells SEQ ID NO: 331.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.

Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 5;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 138
ID   ABB72150 standard; protein; 299 AA.
DE   Human protein isolated from skin cells SEQ ID NO: 189.
PN   WO200190357-A1.
PD   29-NOV-2001.
PA   (GENE.) GENESIS RES & DEV CORP LTD.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 5;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 139
ID   ABB95449 standard; protein; 299 AA.
DE   Human angiogenesis related protein PRO301 SEQ ID NO: 54.
PN   WO200208284-A2.
PD   31-JAN-2002.
PA   (GETH) GENENTECH INC.
PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 5;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 140
ID   ABU71610 standard; protein; 299 AA.
DE   Human PRO polypeptide #21.
PN   US20002146709-A1.
PD   10-OCT-2002.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 6;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 141
ID   ABO17798 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20003032156-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 6;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 142
ID   ABU71465 standard; protein; 299 AA.
DE   Human PRO polypeptide #21.
PN   US200192659-A1.
PD   19-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 6;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 143
ID   ABO25173 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20003040014-A1.
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 6;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 144
ID   ABU81052 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030004311-A1.
PD   02-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 6;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;

RESULT 145
ID   ABU71911 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein PRO301.
PN   US20003003530-A1.
PD   02-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 6;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 146
ID   ABO01794 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US200219767l-A1.
PD   26-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 6;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 147
ID   ABU66752 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20003036180-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 6;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 148
ID   ABU54367 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein PRO301.
PN   US20002132240-A1.
PD   19-SEP-2002.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 6;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 149
ID   ABU67291 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20003032063-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 6;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 150
ID   ABO47382 standard; protein; 299 AA.
DE   Human secreted/transmembrane polypeptide PRO301.
PN   US20003044835-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 6;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 151
ID   ABU59833 standard; protein; 299 AA.
DE   Novel secreted and transmembrane protein PRO301.
PN   US20003017563-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 6;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 152
ID   ABO25023 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein (PRO) #183.
PN   US20003036179-A1.
PD   20-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 6;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 153
ID   ABU64519 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #23.
PN   US20002160374-A1.
PD   31-OCT-2002.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 6;   Length 299;
                        26.5%;   Pred. No. 1.1e-06;
RESULT 154

ID ABU72059 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 155
ID ABU67365 standard; protein; 299 AA.
DE Human secreted protein PRO301.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 156
ID ABU67160 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 157
ID ABO14885 standard; protein; 299 AA.
DE Human secreted / transmembrane polypeptide PRO301.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 158
ID ABU07736 standard; protein; 299 AA.
DE Human A-33 related antigen PRO301.
PN US2002182206-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 159
ID AAO16451 standard; protein; 299 AA.
DE Human junctional adhesion molecule 1 (huJAM1).
PN WO200300541-A2.
PD 30-JAN-2003.
PA (BLIL) LILLY & CO ELI.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 160
ID ABU67028 standard; protein; 299 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 366.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 161
ID ABU69642 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 162
ID ABU79802 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 163
ID ABO14824 standard; protein; 299 AA.

DE Human secreted / transmembrane polypeptide PRO301.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 164
ID ADA45885 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 165
ID ADA76316 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 166
ID ADB29324 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 167
ID ADA18966 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 168
ID ADA61589 standard; protein; 299 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 169
ID ADB19374 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 170
ID ADB27915 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 171
ID ADA86394 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 6; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 172
ID ADB15958 standard; protein; 299 AA.
DE Human PRO polypeptide #183.

PN US20030087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 173
ID ADA47744 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 174
ID ADA18180 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 175
ID ABO32776 standard; protein; 299 AA.
DE Human secreted/transmembrane protein PRO301.
PN US20030045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 176
ID ADA67539 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 177
ID ADB30546 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 178
ID ADA85842 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 179
ID ADA97054 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 180
ID ADA79358 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 181
ID ADA87497 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030087345-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 182
ID ADB16699 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 183
ID ABO34836 standard; protein; 299 AA.
DE Human secreted protein; #21.
PN US20030044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 184
ID ADA16155 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 185
ID ADA91791 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 186
ID ADB14854 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 187
ID ADA47263 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US20030044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 188
ID ADB18815 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 189
ID ADA94030 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
  Query Match   8.5%; Score 178.5; DB 6; Length 299;
  Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 190
ID ADB19926 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030082691-A1.
PD 01-MAY-2003.

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PA     (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 191
ID   ADB13238 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082710-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 192
ID   ABO43331 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030044945-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 193
ID   ADA74492 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030068798-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 194
ID   ADA42200 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030054401-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 195
ID   ADB24725 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US20030077713-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 196
ID   ADB82249 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082701-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 197
ID   ADA75212 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030073216-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 198
ID   ADA85290 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030082695-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 199
ID   ADA84738 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030082708-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.

Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 200
ID   ABO17514 standard; protein; 299 AA.
DE   Human PRO polypeptide #21.
PN   US20030064367-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 201
ID   ADB29994 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030073214-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 202
ID   ADA80522 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082761-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 203
ID   ADA75764 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082703-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 204
ID   ADA46989 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US20030073210-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 205
ID   ADB25285 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030077715-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 206
ID   ADA93461 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030077721-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 207
ID   ADB26811 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030092147-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match                            8.5%;    Score 178.5;  DB 6;  Length 299;
Best Local Similarity     26.5%;    Pred. No. 1.1e-06;
RESULT 208
ID   ADB31098 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030096386-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match
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Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 209
ID   ADA61026 standard; protein; 299 AA.
DE   Homo sapiens.
PN   US20030498I7-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 6;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 210
ID   ADB24173 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US2003077714-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 6;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 211
ID   ADA96502 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003082690-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 6;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 212
ID   ADA81074 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003082702-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 6;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 213
ID   ADA95950 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003082759-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 6;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 214
ID   ADB26259 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003082760-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 6;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 215
ID   ADB21744 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003082765-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 6;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 216
ID   ADA77523 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003068797-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 7;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 217
ID   ADB18263 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003077710-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 7;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;


RESULT 218
ID   ADA86946 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003082709-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 7;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 219
ID   ADA16579 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003039969-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 7;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 220
ID   ADA13008 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003049622-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 7;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 221
ID   ADA41876 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003082540-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 7;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 222
ID   ADA88049 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein, #25.
PN   US2003082700-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 7;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 223
ID   ADA46437 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003054516-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 7;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 224
ID   ADA17223 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003017498-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 7;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 225
ID   ADA42726 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003054351-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 7;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 226
ID   ADB28467 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003082699-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    26.5%;    Score 178.5;  DB 7;  Length 299;
     Best Local Similarity    26.5%;    Pred. No. 1.1e-06;
RESULT 227
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RESULT 228
ID   ADA76971 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030059909-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 229
ID   ADB29019 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082706-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 230
ID   ADA88601 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030073213-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 231
ID   ADA97606 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082686-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 232
ID   ADB27363 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030022239-A1.
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 233
ID   ADB22296 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030087344-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 234
ID   AB019860 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein PRO302.
PN   US20030044902-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 235
ID   AB017575 standard; protein; 299 AA.
DE   Human PRO polypeptide #21.
PN   US20030068793-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 236
ID   ADA66987 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030064923-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

ID   ADB22848 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030077711-A1.

RESULT 237
ID   ADB23621 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US20030077712-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 238
ID   ADA92343 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030082712-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 239
ID   ADB15406 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030087352-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 240
ID   ADB38658 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030082766-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 241
ID   ADB38106 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030087347-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 242
ID   ADB66578 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030082689-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 243
ID   ADB89658 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082698-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 244
ID   ADB90390 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082762-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

RESULT 245
ID   ADB77645 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030077654-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
   Query Match   8.5%;
   Best Local Similarity 26.5%; Score 178.5; DB 7; Length 299; Pred. No. 1.1e-06;

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 246
ID   ADB39491 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030082764-A1.
PD   01-MAY-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 247
ID   ADB74781 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein.
PN   US20030082542-A1.
PD   01-MAY-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 248
ID   ADB47114 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein, #25.
PN   US20030082687-A1.
PD   01-MAY-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 249
ID   ADB86721 standard; protein; 299 AA.
DE   Novel human,secreted and transmembrane protein #183.
PN   US20030082697-A1.
PD   01-MAY-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 250
ID   ADB77326 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20030082696-A1.
PD   01-MAY-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 251
ID   ADB34483 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US20030077717-A1.
PD   24-APR-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 252
ID   ADB35587 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US20030077719-A1.
PD   24-APR-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 253
ID   ADB39931 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US20030077716-A1.
PD   24-APR-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 254
ID   ADB35035 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US20030077718-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match

Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 255
ID   ADB36139 standard; protein; 299 AA.
DE   Human PRO polypeptide SEQ ID NO 366.
PN   US20030077720-A1.
PD   24-APR-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 256
ID   ADB46534 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030082692-A1.
PD   01-MAY-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 257
ID   ADC28427 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030059772-A1.
PD   27-MAR-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 258
ID   ADC39627 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030059828-A1.
PD   27-MAR-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 259
ID   ADC40141 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030059829-A1.
PD   27-MAR-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 260
ID   ADC18969 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030036061-A1.
PD   20-FEB-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 261
ID   ADC34265 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030036094-A1.
PD   20-FEB-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 262
ID   ADC29320 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030049676-A1.
PD   13-MAR-2003.

PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   8.5%;   Score 178.5;   DB 7;
26.5%;   Pred. No. 1.1e-06;   Length 299;
RESULT 263
ID   ADC28851 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20030049677-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match

Best Local Similarity   8.5%;   Score 178.5;   DB 7;

Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 264
ID ADC40736 standard; protein; 299 AA.
PN US20030544400-A1.
DE Human secreted/transmembrane protein, #25.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 265
ID ADC19393 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030544441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 266
ID ADC33841 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 267
ID ADC12911 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 268
ID ADC50407 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 269
ID ADC71954 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 270
ID ADC59933 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 271
ID ADC52940 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US20030087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 272
ID ADC57294 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US20030087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 273
ID ADC60485 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 274
ID ADC50960 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 275
ID ADC65487 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 276
ID ADC54585 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US20030087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 277
ID ADC53546 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US20030087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 278
ID ADC59069 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US20030087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 279
ID ADC55947 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US20030087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 280
ID ADC58517 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein Seq ID366.
PN US20030087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 281
ID ADC12363 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 26.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 282

ID ADO3191 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 283
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADO90183 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
RESULT 284
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADC69602 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
RESULT 285
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADC48491 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
RESULT 286
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADD1020 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 287
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADD04595 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 288
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADC80551 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
RESULT 289
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADD11058 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
RESULT 290
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADD10343 standard; protein; 299 AA.
DE Human secreted/transmembrane PRO polypeptide #27.
PN US20030105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
RESULT 291
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADC47939 standard; protein; 299 AA.

DE Human PRO polypeptide #183.
PN US20030194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
RESULT 292
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADD04918 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
RESULT 293
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADC79999 standard; protein; 299 AA.
DE Novel human secreted and transmembrane PRO polypeptide #27.
PN US20030087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 294
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADD11303 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
RESULT 295
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADD09468 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
RESULT 296
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADD03924 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
RESULT 297
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADD03500 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
RESULT 298
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADD41181 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
RESULT 299
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADD52320 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
RESULT 300
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Pred. No. 1.1e-06; Length 299;

ID ADD53060 standard; protein; 299 AA.
DE Human PRO polypeptide #183.

PN   US20030194792-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 301
ID   ADD37096 standard; protein; 299 AA.
DE   Human secreted/transmembrane PRO polypeptide #27.
PN   US20031050012-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 302
ID   ADD53612 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030203437-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 303
ID   ADD51768 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031947779-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 304
ID   ADD02567 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031203431-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 305
ID   ADD02001 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031203430-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 306
ID   ADD54183 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20030203432-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 307
ID   ADD92500 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031199055-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 308
ID   ADD91396 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031199030-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 309
ID   ADE04010 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031199057-A1.

PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 310
ID   ADE32307 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20031947765-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 311
ID   ADE22239 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031199056-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 312
ID   ADD79463 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031203428-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 313
ID   ADE41999 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031947772-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 314
ID   ADE17816 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031199023-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 315
ID   ADD91948 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20031199053-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 316
ID   ADE33411 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20031947767-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 317
ID   ADE33963 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20031947791-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%;   Score 178.5;   DB 7;
Best Local Similarity   26.5%;   Pred. No. 1.1e-06;   Length 299;

RESULT 318
ID   ADD80015 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032074417-A1.
PD   06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 319
ID ADD93052 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200319476B-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 320
ID ADE19472 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200319905-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 321
ID ADE34752 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US200307583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 322
ID ADE18920 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200319902B-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 323
ID ADE43116 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200319903-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 324
ID ADD95905 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200319905-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 325
ID ADE22791 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200319064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 326
ID ADD78909 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200320342-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 327
ID ADE32859 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US200319476-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 328
ID ADE42551 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200319032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 329
ID ADD80567 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200307418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 330
ID ADD89595 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200319028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 331
ID ADE40879 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200319031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 332
ID ADE04678 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200319034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 333
ID ADE92807 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200319477-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 334
ID ADG21516 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US200307355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 335
ID ADG23157 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US200307384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%; Score 178.5; DB 7; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;
RESULT 336
ID ADF97492 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US200307370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match

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        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 337
ID   ADG80556 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003207373-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 338
ID   ADG80004 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US2003207372-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 339
ID   ADG63772 standard; protein; 299 AA.
DE   Human secreted/transmembrane polypeptide PRO301.
PN   US2003170721-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 340
ID   ADH62528 standard; protein; 299 AA.
DE   Human PRO301 protein.
PN   US2003171568-A1.
PD   11-SEP-2003.
PA   (ASHK/) ASHKENAZI A.
PA   (FONG/) FONG S.
PA   (GODD/) GODDARD A.
PA   (GURN/) GURNEY A L.
PA   (NAPI/) NAPIER M A.
PA   (TUMA/) TUMAS D.
PA   (WOOD/) WOOD W I.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 341
ID   ADH59235 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003039972-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 342
ID   ADH55296 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003207381-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 343
ID   ADH55848 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003207379-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 344
ID   ADI38014 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003054352-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 345
ID   ADI64067 standard; protein; 299 AA.


DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003207385-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 346
ID   ADI65016 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003207386-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 347
ID   ADI63515 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003207387-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 348
ID   ADH81929 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003207388-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 349
ID   ADH81377 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003207377-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 350
ID   ADJ26282 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003054349-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 351
ID   ADM82546 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003087355-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 352
ID   ADN15945 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003087353-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 353
ID   ADN16574 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003087385-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             26.5%;  Score 178.5;  DB 7;  Length 299;
        Best Local Similarity  26.5%;  Pred. No. 1.1e-06;

RESULT 354
ID   ADN15393 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
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PN US20030087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

PN US20030087357-A1.
PD 08-MAY-2003.
DE Novel human secreted and transmembrane protein PRO301.
ID ADN14841 standard; protein; 299 AA.
RESULT 355
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

PD 15-MAY-2003.
PN US20030092115-A1.
DE Novel human secreted and transmembrane protein PRO301.
ID ADC81103 standard; protein; 299 AA.
RESULT 356
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 7; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

PD 17-JUL-2003.
PN US20030135025-A1.
DE Human secreted/transmembrane protein, #25.
ID ADE79197 standard; protein; 299 AA.
RESULT 357
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

PD 29-MAY-2003.
PN US20030100087-A1.
DE Human PRO polypeptide #183.
ID ADD76551 standard; protein; 299 AA.
RESULT 358
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

PD 15-MAY-2003.
PN US20030092113-A1.
DE Human PRO polypeptide #183.
ID ADD87915 standard; protein; 299 AA.
RESULT 359
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

PD 30-OCT-2003.
PN US20030203440-A1.
DE Human PRO polypeptide #183.
ID ADD86319 standard; protein; 299 AA.
RESULT 360
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

PD 15-MAY-2003.
PN US20030130489-A1.
DE Human secreted/transmembrane protein, #25.
ID ADE79621 standard; protein; 299 AA.
RESULT 361
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

PD 10-JUL-2003.
PN US20030211571-A1.
DE Human PRO polypeptide #183.
ID ADE75767 standard; protein; 299 AA.
RESULT 362
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

PD 13-NOV-2003.
PN US20030212592-A1.
DE Human secreted/transmembrane protein, #25.
ID ADE72297 standard; protein; 299 AA.
RESULT 363
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;

PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
RESULT 364
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.
PD 29-MAY-2003.
PN US20030100497-A1.
DE Human secreted/transmembrane PRO polypeptide #27.
ID ADE41304 standard; protein; 299 AA.

RESULT 365
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.
PD 15-MAY-2003.
PN US20030092108-A1.
DE Human PRO polypeptide #183.
ID ADE23343 standard; protein; 299 AA.

RESULT 366
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.
PD 15-MAY-2003.
PN US20030092110-A1.
DE Human PRO polypeptide #183.
ID ADE23895 standard; protein; 299 AA.

RESULT 367
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.
PD 30-OCT-2003.
PN US20030203439-A1.
DE Human PRO polypeptide #183.
ID ADE24538 standard; protein; 299 AA.

RESULT 368
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.
PD 23-OCT-2003.
PN US20030199062-A1.
DE Human PRO polypeptide #183.
ID ADD87363 standard; protein; 299 AA.

RESULT 369
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.
PD 05-JUN-2003.
PN US20030104558-A1.
DE Human PRO polypeptide #183.
ID ADD89229 standard; protein; 299 AA.

RESULT 370
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.
PD 07-AUG-2003.
PN US20030148370-A1.
DE Human secreted/transmembrane polypeptide PRO301.
ID ADE41186 standard; protein; 299 AA.

RESULT 371
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.
PD 16-OCT-2003.
PN US20030194794-A1.
DE Human secreted/transmembrane protein, #25.
ID ADE73832 standard; protein; 299 AA.

RESULT 372
Best Local Similarity 26.5%;
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Pred. No. 1.1e-06;
PD 16-OCT-2003.
PN US20030194794-A1.
DE Human PRO polypeptide #183.
ID ADE18368 standard; protein; 299 AA.

RESULT 373
ID ADE88677 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

RESULT 374
ID ADE99386 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199027-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

RESULT 375
ID ADE94697 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

RESULT 376
ID ADE91108 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

RESULT 377
ID ADE95249 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

RESULT 378
ID ADE93359 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

RESULT 379
ID ADF34940 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

RESULT 380
ID ADE98505 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;
PA (GETH) GENENTECH INC.

RESULT 381
ID ADE92255 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

RESULT 382
ID ADE90556 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;

RESULT 383
ID ADE91703 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;

RESULT 384
ID ADE98932 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;

RESULT 385
ID ADG40402 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;

RESULT 386
ID ADF73796 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;

RESULT 387
ID ADG02282 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;

RESULT 388
ID ADG22068 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;

RESULT 389
ID ADG20138 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;

RESULT 390
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
Query Match 8.5%; Pred. No. 1.1e-06;

ID   ADF98044 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032074422-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 391
ID   ADG24261 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20032074426-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 392
ID   ADF98615 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032080055-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 393
ID   ADG03446 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032207351-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 394
ID   ADF99167 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032207353-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 395
ID   ADG16752 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032207359-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 396
ID   ADG05211 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032207375-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 397
ID   ADG19478 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032207425-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 398
ID   ADF73372 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20031660051-A1.
PD   04-SEP-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 399
ID   ADG13315 standard; protein; 299 AA.

DE   Human PRO polypeptide #183.
PN   US20032207357-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 400
ID   ADG08372 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20032207424-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 401
ID   ADG15542 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032199885-A1.
PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 402
ID   ADF96940 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032207371-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 403
ID   ADG06125 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032207374-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 404
ID   ADG23709 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20032207389-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 405
ID   ADG03998 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20032207423-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 406
ID   ADG24899 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20032207427-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 407
ID   ADG07196 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US20032207350-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity   26.5%; Pred. No. 1.1e-06;

RESULT 408
ID   ADG07748 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.

PN US20030207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 409
ID ADG55243 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20031194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 410
ID ADG60907 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 411
ID ADG62011 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 412
ID ADG92215 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030207145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 413
ID ADG82212 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 414
ID ADG57451 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 415
ID ADG56899 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 416
ID ADG55795 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 417
ID ADG58855 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 418
ID ADG70921 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 419
ID ADG92642 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US20030207146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 420
ID ADG58003 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 421
ID ADG53587 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 422
ID ADG71473 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 423
ID ADG81660 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 424
ID ADH30622 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US20030180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 425
ID ADG63621 standard; protein; 299 AA.
DE Human secreted/transmembrane polypeptide PRO301.
PN US20030207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Pred. No. 1.1e-06;
Best Local Similarity 26.5%; Score 178.5; DB 8; Length 299;
RESULT 426
ID ADH11989 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US20030207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match   8.5%;   Pred. No. 1.1e-06;
Best Local Similarity 26.5%;   Score 178.5;   DB 8;   Length 299;
RESULT 427
ID   ADG52411 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US200320714-A1.
PD   06-NOV-2003;
PA   (GETH) GENENTECH INC.

Query Match   8.5%;   Pred. No. 1.1e-06;
Best Local Similarity 26.5%;   Score 178.5;   DB 8;   Length 299;
RESULT 428
ID   ADG54139 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US200320741-A1.
PD   06-NOV-2003;
PA   (GETH) GENENTECH INC.

Query Match   8.5%;   Pred. No. 1.1e-06;
Best Local Similarity 26.5%;   Score 178.5;   DB 8;   Length 299;
RESULT 429
ID   ADG81108 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US200319479-A1.
PD   16-OCT-2003;
PA   (GETH) GENENTECH INC.

Query Match   8.5%;   Pred. No. 1.1e-06;
Best Local Similarity 26.5%;   Score 178.5;   DB 8;   Length 299;
RESULT 430
ID   ADG56347 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US200320736-A1.
PD   06-NOV-2003;
PA   (GETH) GENENTECH INC.

Query Match   8.5%;   Pred. No. 1.1e-06;
Best Local Similarity 26.5%;   Score 178.5;   DB 8;   Length 299;
RESULT 431
ID   ADH12613 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US200320737-A1.
PD   06-NOV-2003;
PA   (GETH) GENENTECH INC.

Query Match   8.5%;   Pred. No. 1.1e-06;
Best Local Similarity 26.5%;   Score 178.5;   DB 8;   Length 299;
RESULT 432
ID   ADG61459 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US200320742-A1.
PD   06-NOV-2003;
PA   (GETH) GENENTECH INC.

Query Match   8.5%;   Pred. No. 1.1e-06;
Best Local Similarity 26.5%;   Score 178.5;   DB 8;   Length 299;
RESULT 433
ID   ADH28546 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US200302233-A1.
PD   30-JAN-2003;
PA   (GETH) GENENTECH INC.

Query Match   8.5%;   Pred. No. 1.1e-06;
Best Local Similarity 26.5%;   Score 178.5;   DB 8;   Length 299;
RESULT 434
ID   ADG54691 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US200320736-A1.
PD   06-NOV-2003;
PA   (GETH) GENENTECH INC.

Query Match   8.5%;   Pred. No. 1.1e-06;
Best Local Similarity 26.5%;   Score 178.5;   DB 8;   Length 299;
RESULT 435
ID   ADG59731 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US200320736-A1.
PD   06-NOV-2003;
PA   (GETH) GENENTECH INC.
Query Match

Best Local Similarity 26.5%;   Pred. No. 1.1e-06;
RESULT 436
ID   ADH20431 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US200400555-A1.
PD   08-JAN-2004.
PA   (GETH) GENENTECH INC.
Best Local Similarity 26.5%;   Score 178.5;   DB 8;   Length 299;
RESULT 437
ID   ADH43487 standard; protein; 299 AA.
DE   Human PRO polypeptide #27.
PN   US200322498-A1.
PD   04-DEC-2003.
PA   (GETH) GENENTECH INC.

Query Match   8.5%;   Score 178.5;   DB 8;   Length 299;
Best Local Similarity 26.5%;   Pred. No. 1.1e-06;
RESULT 438
ID   ADH07286 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US200400621-A1.
PD   08-JAN-2004.
PA   (GETH) GENENTECH INC.

Query Match   8.5%;   Score 178.5;   DB 8;   Length 299;
Best Local Similarity 26.5%;   Pred. No. 1.1e-06;
RESULT 439
ID   ADH59831 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US200321590-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.

Query Match   8.5%;   Score 178.5;   DB 8;   Length 299;
Best Local Similarity 26.5%;   Pred. No. 1.1e-06;
RESULT 440
ID   ADH06859 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US200400566-A1.
PD   08-JAN-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.

Query Match   8.5%;   Score 178.5;   DB 8;   Length 299;
Best Local Similarity 26.5%;   Pred. No. 1.1e-06;
RESULT 441
ID   ADI81155 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US200320736-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.

Query Match   8.5%;   Score 178.5;   DB 8;   Length 299;
Best Local Similarity 26.5%;   Pred. No. 1.1e-06;
RESULT 442
ID   ADI18601 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US200312999-A1.
PD   14-AUG-2003.
PA   (GETH) GENENTECH INC.

Query Match   8.5%;   Score 178.5;   DB 8;   Length 299;
Best Local Similarity 26.5%;   Pred. No. 1.1e-06;
RESULT 443
ID   ADI65321 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US200314881-A1.

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PD   07-AUG-2003.
PA   (GETH ) GENENTECH INC.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 444
ID   ADI37584 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003096340-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 445
ID   ADG09898 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2004009548-A1.
PD   15-JAN-2004.
PA   (GETH ) GENENTECH INC.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 446
ID   ADH97380 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003207382-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 447
ID   ADI15369 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003190610-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 448
ID   ADG09246 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2004009547-A1.
PD   15-JAN-2004.
PA   (GETH ) GENENTECH INC.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 449
ID   ADI65748 standard; protein; 299 AA.
DE   Human secreted and transmembrane protein, #25.
PN   US2003148371-A1.
PD   07-AUG-2003.
PA   (GETH ) GENENTECH INC.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 450
ID   ADI14701 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003207383-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 451
ID   ADH60491 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2004023331-A1.
PD   05-FEB-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;


Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 452
ID   ADI18296 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2003207349-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 453
ID   ADJ99548 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003187238-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 454
ID   ADL08741 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003186358-A1.
PD   02-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 455
ID   ADI47176 standard; protein; 299 AA.
DE   Human JAM-1 protein sequence.
PN   WO2004003145-A2.
PD   08-JAN-2004.
PA   (NAST-) NASTECH PHARM CO INC.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 456
ID   ADM25082 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003096233-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 457
ID   ADK40844 standard; protein; 299 AA.
DE   Human platelet F11 receptor #1.
PN   US6699888-B1.
PD   02-MAR-2004.
PA   (UTNY-) UNIV NEW YORK STATE RES FOUND.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 458
ID   ADJ63577 standard; protein; 299 AA.
DE   Novel human secreted and transmembrane protein PRO301.
PN   US2004039164-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 459
ID   ADM29832 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US2003190611-A1.
PD   09-OCT-2003.
PA   (GETH ) GENENTECH INC.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
Best Local Similarity  26.5%;   Pred. No. 1.1e-06;

RESULT 460
ID   ADL77818 standard; protein; 299 AA.
DE   Albumin fusion protein related therapeutic protein X, SEQ ID No 1300.
PN   US2004010134-A1.
PD   15-JAN-2004.
PA   (ROSE/) ROSEN C A.
PA   (HASE/) HASELTINE W A.
Query Match     8.5%;   Score 178.5;  DB 8;  Length 299;
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RESULT 461
Best Local Similarity    26.5%;   Score 178.5;   DB 8;   Length 299;
ID   ADL77819 standard; protein; 299 AA.
DE   Albumin fusion protein related therapeutic protein X, SEQ ID No 1301.
PN   US20040010134-A1.
PD   15-JAN-2004.
PA   (ROSE/) ROSEN C A.
PA   (HASE/) HASELTINE W A.
Query Match    8.5%;   Best Local Similarity    26.5%;   Pred. No. 1.1e-06;

RESULT 462
Best Local Similarity    26.5%;   Score 178.5;   DB 8;   Length 299;
ID   ADJ77472 standard; protein; 299 AA.
DE   Human PRO polypeptide #27.
PN   US20040038336-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
Query Match    8.5%;   Best Local Similarity    26.5%;   Pred. No. 1.1e-06;

RESULT 463
Best Local Similarity    26.5%;   Score 178.5;   DB 8;   Length 299;
ID   ADK82832 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20040043927-A1.
PD   04-MAR-2004.
PA   (GETH ) GENENTECH INC.
Query Match    8.5%;   Best Local Similarity    26.5%;   Pred. No. 1.1e-06;

RESULT 464
Best Local Similarity    26.5%;   Score 178.5;   DB 8;   Length 299;
ID   ADJ65594 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20040038335-A1.
PD   26-FEB-2004.
PA   (GETH ) GENENTECH INC.
Query Match    8.5%;   Best Local Similarity    26.5%;   Pred. No. 1.1e-06;

RESULT 465
Best Local Similarity    26.5%;   Score 178.5;   DB 8;   Length 299;
ID   ADL31132 standard; protein; 299 AA.
DE   Human protein encoded by a full length cDNA clone SeqID 3365.
PN   EP1396543-A2.
PD   10-MAR-2004.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match    8.5%;   Best Local Similarity    26.5%;   Pred. No. 1.1e-06;

RESULT 466
Best Local Similarity    26.5%;   Score 178.5;   DB 8;   Length 299;
ID   ADM27730 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20040048333-A1.
PD   11-MAR-2004.
PA   (GETH ) GENENTECH INC.
Query Match    8.5%;   Best Local Similarity    26.5%;   Pred. No. 1.1e-06;

RESULT 467
Best Local Similarity    26.5%;   Score 178.5;   DB 8;   Length 299;
ID   ADL26800 standard; protein; 299 AA.
DE   Human JAM1 protein SEQ ID NO:54.
PN   WO2004022778-A1.
PD   18-MAR-2004.
PA   (GARV-) GARVAN INST MEDICAL RES.
Query Match    8.5%;   Best Local Similarity    26.5%;   Pred. No. 1.1e-06;

RESULT 468
Best Local Similarity    26.5%;   Score 178.5;   DB 8;   Length 299;
ID   ADM42454 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20040058424-A1.
PD   25-MAR-2004.
PA   (GETH ) GENENTECH INC.
Query Match    8.5%;   Best Local Similarity    26.5%;   Pred. No. 1.1e-06;

RESULT 469
Best Local Similarity    26.5%;   Score 178.5;   DB 8;   Length 299;
ID   ADO06154 standard; protein; 299 AA.
DE   Human PRO polypeptide #21.
PN   US6866451-B1.
PD   03-FEB-2004.
PA   (GETH ) GENENTECH INC.
Query Match    8.5%;   Best Local Similarity    26.5%;   Pred. No. 1.1e-06;

RESULT 470
Best Local Similarity    26.5%;   Score 178.5;   DB 8;   Length 299;
ID   ADN35284 standard; protein; 299 AA.
DE   Human PRO301 protein.
PN   WO2004031105-A2.
PD   15-APR-2004.
PA   (GETH ) GENENTECH INC.
Query Match    8.5%;   Best Local Similarity    26.5%;   Pred. No. 1.1e-06;

RESULT 471
Best Local Similarity    26.5%;   Score 178.5;   DB 8;   Length 299;
ID   ADN05140 standard; protein; 299 AA.
DE   Antipsoriatic protein sequence #749.
PN   WO2004028479-A2.
PD   08-APR-2004.
PA   (GETH ) GENENTECH INC.
Query Match    8.5%;   Best Local Similarity    26.5%;   Pred. No. 1.1e-06;

RESULT 472
Best Local Similarity    26.5%;   Score 178.5;   DB 8;   Length 299;
ID   ADM28316 standard; protein; 299 AA.
DE   Human PRO polypeptide #183.
PN   US20040077064-A1.
PD   22-APR-2004.
PA   (GETH ) GENENTECH INC.
Query Match    8.5%;   Best Local Similarity    26.5%;   Pred. No. 1.1e-06;

RESULT 473
Best Local Similarity    26.5%;   Score 178.5;   DB 8;   Length 299;
ID   ADQ95890 standard; protein; 299 AA.
DE   T cell activation associated protein #34.
PN   WO2004058805-A2.
PD   15-JUL-2004.
PA   (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match    8.5%;   Best Local Similarity    26.5%;   Pred. No. 1.1e-06;

RESULT 474
Best Local Similarity    26.5%;   Score 178.5;   DB 8;   Length 299;
ID   ADR11006 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20040137561-A1.
PD   15-JUL-2004.
PA   (GETH ) GENENTECH INC.
Query Match    8.5%;   Best Local Similarity    26.5%;   Pred. No. 1.1e-06;

RESULT 475
Best Local Similarity    26.5%;   Score 178.5;   DB 8;   Length 299;
ID   ADR17915 standard; protein; 299 AA.
DE   Human secreted/transmembrane protein, #25.
PN   US20040147017-A1.
PD   29-JUL-2004.
PA   (ASHK/) ASHKENAZI A.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAOW/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GRIM/) GRIMALDI C J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (MATH/) MATHER J P.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Query Match    8.5%;   Best Local Similarity    26.5%;   Pred. No. 1.1e-06;

RESULT 476
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ID ADR27641 standard; protein; 299 AA.
DE Human F11 receptor protein Seq 7.
PN WO2004063327-A2.
PD 29-JUL-2004.
PA (KORN/) KORNECKI E.
PA (BABI/) BABINSKA A.
PA (EHRL/) EHRLICH Y H.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 477
ID ADI95798 standard; protein; 299 AA.
DE Human PRO polypeptide #183.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 478
ID ADI96350 standard; protein; 299 AA.
DE Novel human secreted and transmembrane protein PRO301.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 479
ID ADR46577 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4, SEQ ID 8.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 480
ID ADR46571 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 481
ID ADR46573 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 4.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 482
ID ADR46579 standard; protein; 299 AA.
DE Human JAM-1, F11 receptor (F11R) transcript variant 5.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 483
ID ADT03591 standard; protein; 299 AA.
DE Human secreted/transmembrane protein, #25.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 484
ID ADT94260 standard; protein; 299 AA.
DE Human PRO301 protein.
PN AU2003259607-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 485
ID ADS74554 standard; protein; 299 AA.
DE Human secreted/transmembrane protein #25.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 8.5%; Score 178.5; DB 8; Length 299;
Best Local Similarity 26.5%; Pred. No. 1.1e-06;

RESULT 486
ID ADE09073 standard; protein; 320 AA.
DE Novel protein-related contig polypeptide sequence #139.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 8.5%; Score 178.5; DB 7; Length 320;
Best Local Similarity 26.5%; Pred. No. 1.2e-06;

RESULT 487
ID ADJ67616 standard; protein; 335 AA.
DE Human ovarian specific polypeptide SEQ ID NO:330.
PN WO2004013311-A2.
PD 12-FEB-2004.
PA (DIAD-) DIADEXUS INC.
Query Match 8.5%; Score 178.5; DB 7; Length 335;
Best Local Similarity 26.5%; Pred. No. 1.3e-06;

RESULT 488
ID ADE08038 standard; protein; 336 AA.
DE Novel protein (useful for identifying genetic disorders) #193.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 8.5%; Score 178.5; DB 7; Length 336;
Best Local Similarity 26.5%; Pred. No. 1.3e-06;

RESULT 489
ID ADQ89964 standard; protein; 34350 AA.
DE Antagonist of cell cycle progression polypeptide #197.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 8.5%; Score 178; DB 8; Length 34350;
Best Local Similarity 24.2%; Pred. No. 0.0011;

RESULT 490
ID AAW14146 standard; protein; 319 AA.
DE Human A33 antigen.
PN WO9708189-A1.
PD 06-MAR-1997.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 8.4%; Score 177; DB 2; Length 319;
Best Local Similarity 27.5%; Pred. No. 1.6e-06;

RESULT 491
ID AAY23323 standard; protein; 319 AA.

DE Amino acid sequence of the A33 antigen.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
RESULT 492
    Query Match   8.4%;   Score 177;   DB 2;   Length 319;
    Best Local Similarity   27.5%;   Pred. No. 1.6e-06;
ID AAB65863 standard; protein; 319 AA.
DE Human A33 protein SEQ ID NO: 67.
PN WO200078808-A1.
PD 28-DEC-2000.
PA (MILL-) MILLENNIUM PHARM INC.
    Query Match   8.4%;   Score 177;   DB 4;   Length 319;
    Best Local Similarity   27.5%;   Pred. No. 1.6e-06;
RESULT 493
ID ADA10947 standard; protein; 319 AA.
DE Human cDNA differentially expressed in colon cancer #43 product.
PN US2002160382-A1.
PD 31-OCT-2002;
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
RESULT 494
    Query Match   8.4%;   Score 177;   DB 6;   Length 319;
    Best Local Similarity   27.5%;   Pred. No. 1.6e-06;
ID ADH62533 standard; protein; 319 AA.
DE Human A33 antigenic protein.
PN US2003171568-A1.
PD 11-SEP-2003;
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
RESULT 495
    Query Match   8.4%;   Score 177;   DB 7;   Length 319;
    Best Local Similarity   27.5%;   Pred. No. 1.6e-06;
ID ADN39847 standard; protein; 319 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C217.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB/) EOS BIOTECHNOLOGY INC.
RESULT 496
    Query Match   8.4%;   Score 177;   DB 7;   Length 319;
    Best Local Similarity   27.5%;   Pred. No. 1.6e-06;
ID ADN35289 standard; protein; 319 AA.
DE Human A33 antigen protein.
PN WO2004031105-A2.
PD 15-APR-2004;
PA (GETH) GENENTECH INC.
RESULT 497
    Query Match   8.4%;   Score 177;   DB 8;   Length 319;
    Best Local Similarity   27.5%;   Pred. No. 1.6e-06;
ID ADP54587 standard; protein; 319 AA.
DE Human PRO protein sequence SEQ ID NO:563.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
RESULT 498
    Query Match   8.4%;   Score 177;   DB 8;   Length 319;
    Best Local Similarity   27.5%;   Pred. No. 1.6e-06;
ID ABP62081 standard; protein; 336 AA.
DE Human polypeptide SEQ ID NO 318.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
RESULT 499
    Query Match   8.4%;   Score 177;   DB 5;   Length 336;
    Best Local Similarity   27.5%;   Pred. No. 1.7e-06;
ID ADC78439 standard; protein; 299 AA.
DE Human PRO301 protein.
PN WO200015796-A2.

PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
    Query Match   8.4%;   Score 176.5;   DB 3;   Length 299;
    Best Local Similarity   26.5%;   Pred. No. 1.5e-06;
RESULT 500
ID AAY08073 standard; protein; 268 AA.
DE Human A33 protein.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
    Query Match   8.4%;   Score 176;   DB 2;   Length 268;
    Best Local Similarity   27.7%;   Pred. No. 1.5e-06;
RESULT 501
ID ADH62551 standard; protein; 268 AA.
DE Human A33 antigenic protein fragment #1.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
RESULT 502
    Query Match   8.4%;   Score 176;   DB 7;   Length 270;
    Best Local Similarity   27.7%;   Pred. No. 1.6e-06;
ID AAY23327 standard; protein; 270 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
RESULT 503
    Query Match   8.4%;   Score 176;   DB 2;   Length 273;
    Best Local Similarity   27.7%;   Pred. No. 1.6e-06;
ID AAY23329 standard; protein; 273 AA.
DE An A33 related antigen sequence.
PN WO9927098-A2.
PD 03-JUN-1999.
PA (GETH) GENENTECH INC.
RESULT 504
    Query Match   8.4%;   Score 176;   DB 2;   Length 273;
    Best Local Similarity   27.7%;   Pred. No. 1.6e-06;
ID AAY08075 standard; protein; 273 AA.
DE Human A33 protein fragment #2.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
RESULT 505
    Query Match   8.4%;   Score 176;   DB 2;   Length 273;
    Best Local Similarity   27.7%;   Pred. No. 1.6e-06;
ID ADH62553 standard; protein; 273 AA.
DE Human A33 antigenic protein fragment #2.
PN US2003171568-A1.
PD 11-SEP-2003.
PA (ASHK/) ASHKENAZI A.
PA (FONG/) FONG S.
PA (GODD/) GODDARD A.
PA (GURN/) GURNEY A L.
PA (NAPI/) NAPIER M A.
PA (TUMA/) TUMAS D.
PA (WOOD/) WOOD W I.
RESULT 506
    Query Match   8.4%;   Score 176;   DB 7;   Length 273;
    Best Local Similarity   27.7%;   Pred. No. 1.6e-06;
ID ADH80722 standard; protein; 301 AA.
DE Human polypeptide #39.
PN US2003232054-A1.
PD 18-DEC-2003.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (CHEN/) CHEN R.

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PA   (QIAN/) QIAN X B.
PA   (WANG/) WANG Z W.
PA   (WEHR/) WEHRMAN T.
PA   (ZHAN/) ZHANG J.
PA   (ZHOU/) ZHOU P.
PA   (CAOY/) CAO Y.
PD   02-MAR-2004.
PA   (DRMA/) DRMANAC R T.
PA   (UYNY ) UNIV NEW YORK STATE RES FOUND.

RESULT 507
        Query Match             8.3%;  Score  173.5;  DB 8;  Length 301;
        Best Local Similarity   26.6%;  Pred. No. 3e-06;

ID   ADK40854 standard; protein; 316 AA.
DE   Human A33 molecule.
PN   US6699688-B1.
PD   02-MAR-2004.

RESULT 508
        Query Match             8.2%;  Score  172.5;  DB 8;  Length 316;
        Best Local Similarity   26.4%;  Pred. No. 3.9e-06;

ID   AAY23326 standard; protein; 260 AA.
DE   An A33 related antigen sequence.
PN   WO9927098-A2.
PD   03-JUN-1999.
PA   (GETH ) GENENTECH INC.

RESULT 509
        Query Match             8.1%;  Score  169.5;  DB 2;  Length 260;
        Best Local Similarity   26.1%;  Pred. No. 5.3e-06;

ID   AAY08072 standard; protein; 260 AA.
DE   Human DNA40628 protein.
PN   WO9914241-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.
PA   (ASHK/) ASHKENAZI A.
PA   (FONG/) FONG S.
PA   (GODD/) GODDARD A.
PA   (GURN/) GURNEY A L.
PA   (NAPI/) NAPIER M A.
PA   (TUMA/) TUMAS D.
PA   (WOOD/) WOOD W I.

RESULT 510
        Query Match             8.1%;  Score  169.5;  DB 7;  Length 260;
        Best Local Similarity   26.1%;  Pred. No. 5.3e-06;

ID   ADH62550 standard; protein; 260 AA.
DE   Human PRO301 protein fragment #1.
PN   US2003171568-A1.
PD   11-SEP-2003.

RESULT 511
        Query Match             8.1%;  Score  169.5;  DB 2;  Length 263;
        Best Local Similarity   26.1%;  Pred. No. 5.4e-06;

ID   AAY23328 standard; protein; 263 AA.
DE   An A33 related antigen sequence.
PN   WO9927098-A2.
PD   03-JUN-1999.
PA   (GETH ) GENENTECH INC.

RESULT 512
        Query Match             8.1%;  Score  169.5;  DB 2;  Length 263;
        Best Local Similarity   26.1%;  Pred. No. 5.4e-06;

ID   AAY08074 standard; protein; 263 AA.
DE   Human DNA40628 protein fragment #2.
PN   WO9914241-A2.
PD   25-MAR-1999.
PA   (GETH ) GENENTECH INC.
PA   (FONG/) FONG S.
PA   (GODD/) GODDARD A.
PA   (GURN/) GURNEY A L.
PA   (NAPI/) NAPIER M A.
PA   (TUMA/) TUMAS D.
PA   (WOOD/) WOOD W I.

RESULT 513
        Query Match             8.1%;  Score  169.5;  DB 2;  Length 263;
        Best Local Similarity   26.1%;  Pred. No. 5.4e-06;

ID   ADH62552 standard; protein; 263 AA.
DE   Human PRO301 protein fragment #2.
PN   US2003171568-A1.
PD   11-SEP-2003.
PA   (ASHK/) ASHKENAZI A.
PA   (FONG/) FONG S.
PA   (GODD/) GODDARD A.
PA   (GURN/) GURNEY A L.
PA   (NAPI/) NAPIER M A.


PA   (TUMA/) TUMAS D.
PA   (WOOD/) WOOD W I.
        Query Match             8.1%;  Score  169.5;  DB 7;  Length 263;
        Best Local Similarity   26.1%;  Pred. No. 5.4e-06;

RESULT 514
ID   ADK46581 standard; protein; 300 AA.
DE   Mouse junctional adhesion molecule-1, SEQ ID 12.
PN   JP2004242513-A.
PD   02-SEP-2004.
PA   (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.

RESULT 515
        Query Match             8.0%;  Score  168;  DB 8;  Length 300;
        Best Local Similarity   24.8%;  Pred. No. 8.8e-06;

ID   AAW61379 standard; protein; 298 AA.
DE   Human junctional adhesion molecule protein.
PN   WO9824897-A1.
PD   11-JUN-1998.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.

RESULT 516
        Query Match             8.0%;  Score  167;  DB 2;  Length 298;
        Best Local Similarity   24.8%;  Pred. No. 1.1e-05;

ID   AAW61380 standard; protein; 300 AA.
DE   Mouse junctional adhesion molecule protein.
PN   WO9824897-A1.
PD   11-JUN-1998.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.

RESULT 517
        Query Match             8.0%;  Score  167;  DB 2;  Length 300;
        Best Local Similarity   24.8%;  Pred. No. 1.1e-05;

ID   AAY23325 standard; protein; 300 AA.
DE   A33 related antigen JAM.
PN   WO9927098-A2.
PD   03-JUN-1999.
PA   (GETH ) GENENTECH INC.

RESULT 518
        Query Match             8.0%;  Score  167;  DB 2;  Length 300;
        Best Local Similarity   24.8%;  Pred. No. 1.1e-05;

ID   ADH62537 standard; protein; 300 AA.
DE   Murine JAM protein used in the exemplification of the invention.
PN   US2003171568-A1.
PD   11-SEP-2003.
PA   (ASHK/) ASHKENAZI A.
PA   (FONG/) FONG S.
PA   (GODD/) GODDARD A.
PA   (GURN/) GURNEY A L.
PA   (NAPI/) NAPIER M A.
PA   (TUMA/) TUMAS D.
PA   (WOOD/) WOOD W I.

RESULT 519
        Query Match             8.0%;  Score  167;  DB 7;  Length 300;
        Best Local Similarity   24.8%;  Pred. No. 1.1e-05;

ID   ADK40853 standard; protein; 300 AA.
DE   Mouse junction adhesion molecule (JAM).
PN   US6699688-B1.
PD   02-MAR-2004.
PA   (UYNY ) UNIV NEW YORK STATE RES FOUND.

RESULT 520
        Query Match             8.0%;  Score  167;  DB 8;  Length 300;
        Best Local Similarity   24.8%;  Pred. No. 1.1e-05;

ID   ADN35293 standard; protein; 300 AA.
DE   Human JAM protein.
PN   WO2004031105-A2.
PD   15-APR-2004.
PA   (GETH ) GENENTECH INC.

RESULT 521
        Query Match             8.0%;  Score  167;  DB 8;  Length 300;
        Best Local Similarity   24.8%;  Pred. No. 1.1e-05;

ID   ABB83928 standard; protein; 365 AA.
DE   pCAR SEQ ID NO 4.
PN   US2002059654-A1.
PD   16-MAY-2002.
PA   (BUHL/) BUHLER T.
PA   (GADI/) GADIENT R A.
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RESULT 522
     Query Match
     Best Local Similarity   8.0%;   Score 167; DB 5;    Length 365;
                                     Pred. No. 1.4e-05;
PA   (KORN/) KORN R.
PA   (MOVV/) MOVVA R.
PD   27-DEC-2002.
PN   WO200210335S-A1.

RESULT 523
     Query Match
     Best Local Similarity   22.3%;  Score 164.5; DB 6;  Length 31267;
                                     Pred. No. 0.014;
ID   ABG74786 standard; protein; 31267 AA.
DE   Human RGS11 protein.
PN   WO2002103355-A1.
PD   27-DEC-2002.
PA   (TAKE ) TAKEDA CHEM IND LTD.

RESULT 524
     Query Match
     Best Local Similarity   22.2%;  Score 164; DB 2;    Length 318;
                                     Pred. No. 2.1e-05;
ID   AAW14158 standard; protein; 318 AA.
DE   Mouse A33 antigen.
PN   WO9708189-A1.
PD   06-MAR-1997.
PA   (LUDW-) LUDWIG INST CANCER RES.

RESULT 525
     Query Match
     Best Local Similarity   27.7%;  Score 163.5; DB 5;  Length 261;
                                     Pred. No. 1.8e-05;
ID   AAB83927 standard; protein; 261 AA.
DE   C-terminally truncated pCAR SEQ ID NO 2.
PN   US2002059654-A1.
PD   16-MAY-2002.

RESULT 526
     Query Match
     Best Local Similarity   7.8%;   Score 163; DB 5;    Length 280;
ID   AAB39253 standard; protein; 280 AA.
DE   Gene 15 human secreted protein homologous amino acid sequence #133.
PN   WO200056754-A1.
PD   28-SEP-2000.
PA   (HUMA-) HUMAN GENOME SCI INC.

RESULT 527
     Query Match
     Best Local Similarity   24.7%;  Score 160; DB 3;    Length 280;
                                     Pred. No. 3.9e-05;
ID   AAY72878 standard; protein; 352 AA.
DE   Human PRO5723 protein encoded by DNA82361 cDNA clone.
PN   WO200116319-A2.
PD   08-MAR-2001.

RESULT 528
     Query Match
     Best Local Similarity   7.6%;   Score 159; DB 4;    Length 352;
                                     Pred. No. 6.6e-05;
ID   AAB50930 standard; protein; 352 AA.
DE   Human PRO5723 protein.
PN   WO200073452-A2.
PD   07-DEC-2000.
PA   (GETH ) GENENTECH INC.

RESULT 529
     Query Match
     Best Local Similarity   23.2%;  Score 159; DB 4;    Length 352;
                                     Pred. No. 6.6e-05;
ID   AAB65294 standard; protein; 352 AA.
DE   Human PRO5723 protein sequence SEQ ID NO:505.
PN   WO200073454-A1.
PD   07-DEC-2000.
PA   (GETH ) GENENTECH INC.

RESULT 530
     Query Match
     Best Local Similarity   7.6%;   Score 159; DB 4;    Length 352;
                                     Pred. No. 6.6e-05;
ID   ABB84956 standard; protein; 352 AA.
DE   Human PRO5723 protein sequence SEQ ID NO:280.
PN   WO200090690-A2.
PD   03-JAN-2002.
PA   (GETH ) GENENTECH INC.

RESULT 531
     Query Match
     Best Local Similarity   7.6%;   Score 159; DB 5;    Length 352;
                                     Pred. No. 6.6e-05;
ID   ABB95562 standard; protein; 352 AA.
DE   Human angiogenesis related protein PRO5723 SEQ ID NO: 280.
PN   WO200209284-A2.
PD   31-JAN-2002.
PA   (GETH ) GENENTECH INC.
ID   ABU58109 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US2003027163-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.

RESULT 532
     Query Match
     Best Local Similarity   7.6%;   Score 159; DB 6;    Length 352;
                                     Pred. No. 6.6e-05;
ID   ABU59187 standard; protein; 352 AA.
DE   Novel human secreted or transmembrane protein PRO5723.
PN   US2002132252-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.

RESULT 533
     Query Match
     Best Local Similarity   23.2%;  Score 159; DB 6;    Length 352;
                                     Pred. No. 6.6e-05;
ID   ABU82699 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003032023-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.

RESULT 534
     Query Match
     Best Local Similarity   23.2%;  Score 159; DB 6;    Length 352;
                                     Pred. No. 6.6e-05;
ID   ABU60618 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein, #177.
PN   US2002160384-A1.
PD   31-OCT-2002.
PA   (GETH ) GENENTECH INC.

RESULT 535
     Query Match
     Best Local Similarity   23.2%;  Score 159; DB 6;    Length 352;
                                     Pred. No. 6.6e-05;
ID   ABU80846 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003036635-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.

RESULT 536
     Query Match
     Best Local Similarity   7.6%;   Score 159; DB 6;    Length 352;
                                     Pred. No. 6.6e-05;
ID   ABQ33812 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003045687-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.

RESULT 537
     Query Match
     Best Local Similarity   23.2%;  Score 159; DB 5;    Length 352;
                                     Pred. No. 6.6e-05;
ID   ABU14000 standard; protein; 352 AA.
DE   Human PRO5723 polypeptide.
PN   US2002103125-A1.
PD   01-AUG-2002.
PA   (GETH ) GENENTECH LTD.
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Additional applicant/inventor fields appearing in the listing:

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PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
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RESULT 538
ID ABU72585 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200303531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 539
ID ABG74762 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN US200192752-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 540
ID ABU59334 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, #177.
PN US2003027162-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 541
ID ABO26031 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 542
ID ABU82155 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200308063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 543
ID ABU59040 standard; protein; 352 AA.
DE Human secreted/transmembrane protein.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 544
ID ABU92418 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US200322187-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 545
ID ABU59483 standard; protein; 352 AA.
DE Novel human secreted or transmembrane protein PRO3301.
PN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 546
ID ABU92249 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003017476-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 547
ID ABU10955 standard; protein; 352 AA.
DE Human PRO polypeptide #141.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 548
ID ABU81707 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 549
ID ABU88646 standard; protein; 352 AA.
DE Human secreted and transmembrane polypeptide PRO5723.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 550
ID ABO34160 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 551
ID ABU72335 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 552
ID ADA38016 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 553
ID ADA21702 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO5723.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 554
ID ADA10489 standard; protein; 352 AA.
DE Human secreted/transmembrane protein, PRO5723.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 555
ID ADA18033 standard; protein; 352 AA.
DE Human PRO5723 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 556
ID ADA28141 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity   7.6%;   Score 159;   DB 6;   Length 352;
                         23.2%; Pred. No. 6.6e-05;

RESULT 557

ID ADA94721 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 6; Length 352;

RESULT 558
ID ADA38946 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 6; Length 352;

RESULT 559
ID ADA93067 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 6; Length 352;

RESULT 560
ID ABJ72463 standard; protein; 352 AA.
DE Human PRO5723 protein.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 6; Length 352;

RESULT 561
ID ABO34358 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 6; Length 352;

RESULT 562
ID ABO53246 standard; protein; 352 AA.
DE Human secreted/transmembrane polypeptide PRO 5723.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 6; Length 352;

RESULT 563
ID ADA22628 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003040473-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 6; Length 352;

RESULT 564
ID ABO22616 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 7; Length 352;

RESULT 565
ID ADA06794 standard; protein; 352 AA.
DE Human secreted/transmembrane PRO polypeptide #141.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 7; Length 352;

RESULT 566
ID ABJ72165 standard; protein; 352 AA.
DE Human membrane bound receptor/protein PRO5723 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 7; Length 352;

RESULT 567

ID ADA39487 standard; protein; 352 AA.
DE Human secreted/transmembrane protein PRO5723.
PN US2003059782-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 7; Length 352;

RESULT 568
ID ADB80812 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 7; Length 352;

RESULT 569
ID ADB83706 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 7; Length 352;

RESULT 570
ID ADB73353 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003069968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 7; Length 352;

RESULT 571
ID ADB96513 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 7; Length 352;

RESULT 572
ID ADB78435 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 7; Length 352;

RESULT 573
ID ADB85083 standard; protein; 352 AA.
DE Novel human PRO polypeptide #108.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 7; Length 352;

RESULT 574
ID ADB78189 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 7; Length 352;

RESULT 575
ID ADB87255 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003080067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 23.2%; Score 159; Pred. No. 6.6e-05; DB 7; Length 352;

RESULT 576
ID ADB84837 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US2003092890-A1.

PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 577
ID   ADB83952 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003069397-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 578
ID   ADB73107 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003092887-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 579
ID   ADC57985 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US2003027754-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 580
ID   ADC55349 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US2003045463-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 581
ID   ADC12216 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003049681-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 582
ID   ADC56638 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US2003064375-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 583
ID   ADC11683 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003069403-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 584
ID   ADC36945 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003088065-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 585
ID   ADC21935 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003096969-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 586
ID   ADC49966 standard; protein; 352 AA.

DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003088064-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 587
ID   ADC49165 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003088070-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 588
ID   ADC49682 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003088071-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 589
ID   ADC47543 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003088072-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 590
ID   ADC14805 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003082546-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 591
ID   ADC47288 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003105288-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 592
ID   ADD08337 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003068623-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 593
ID   ADC82162 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US2003083461-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 594
ID   ADD07804 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2002193299-A1.
PD   19-DEC-2002.
PA   (GETH) GENENTECH INC.

     Query Match   23.2%; Score 159; DB 7; Length 352;
     Best Local Similarity   7.6%; Pred. No. 6.6e-05;
RESULT 595
ID   ADC78163 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003096972-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.

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Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 596
ID   ADC82695 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US2003059833-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 597
ID   ADD06398 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003073816-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 598
ID   ADD10569 standard; protein; 352 AA.
DE   Human secreted/transmembrane PRO polypeptide #140.
PN   US2003105011-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 599
ID   ADD08875 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003073090-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 600
ID   ADC77917 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003088066-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 601
ID   ADD07124 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2002193300-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 602
ID   ADD11529 standard; protein; 352 AA.
DE   Human secreted/transmembrane PRO polypeptide #140.
PN   US2003105013-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 603
ID   ADC83371 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US2003059783-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 604
ID   ADD50080 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003105291-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 605
ID   ADD15380 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003059437-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 606
ID   ADD51126 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003105290-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 607
ID   ADD55478 standard; protein; 352 AA.
DE   Human secreted/transmembrane PRO polypeptide #141.
PN   US2003077593-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 608
ID   ADD37322 standard; protein; 352 AA.
DE   Human secreted/transmembrane PRO polypeptide #140.
PN   US2003105012-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 609
ID   ADD56436 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003075594-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 610
ID   ADD50607 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003096971-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 611
ID   ADD54874 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US2002132253-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 612
ID   ADD50361 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003096970-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 613
ID   ADD51372 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003105289-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Score  159;  DB 7;  Length 352;
Best Local Similarity  23.2%;                       Pred. No. 6.6e-05;

RESULT 614
ID   ADB31893 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003068647-A1.
PD   10-APR-2003.
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RESULT 615
Query Match   7.6%;   Score 159; DB 7; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADE27028 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003087304-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 616
Query Match   7.6%;   Score 159; DB 7; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADE26495 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003087305-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 617
Query Match   7.6%;   Score 159; DB 7; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADF67432 standard; protein; 352 AA.
DE   Human PRO5723 amino acid sequence SEQ ID NO:505.
PN   US2002198148-A1.
PD   26-DEC-2002.
PA   (GETH) GENENTECH INC.

RESULT 618
Query Match   7.6%;   Score 159; DB 7; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADE94085 standard; protein; 352 AA.
DE   Immune disease treatment/diagnosis related PRO5723.
PN   US2003082199-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 619
Query Match   7.6%;   Score 159; DB 7; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADI35686 standard; protein; 352 AA.
DE   Human PRO polypeptide #141.
PN   US2003050457-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.

RESULT 620
Query Match   7.6%;   Score 159; DB 7; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADI00179 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003049682-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 621
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADC48919 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003092888-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 622
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADE21090 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100735-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 623
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADE05934 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100728-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 624
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADE75163 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100712-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 625
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADD75909 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100717-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 626
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADD85141 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100722-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 627
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADD86967 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100734-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 628
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADE20844 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100738-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 629
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADE39141 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003096362-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 630
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADE05688 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100727-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 631
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADD73673 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100711-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 632
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADD78513 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100737-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 633
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity 23.2%;   Pred. No. 6.6e-05;
ID   ADE41530 standard; protein; 352 AA.
DE   Human secreted/transmembrane PRO polypeptide #140.
PN   US2003100497-A1.
DE   Human PRO polypeptide #108.

PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 634
ID   ADE21336 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100736-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 635
ID   ADE77451 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100732-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 636
ID   ADE20598 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100733-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 637
ID   ADE75663 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100064-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 638
ID   ADE74179 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100708-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 639
ID   ADD74425 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100709-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 640
ID   ADD76155 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100718-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 641
ID   ADD85647 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100721-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 642
ID   ADE05196 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100726-A1.
PD   29-MAY-2003.

PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 643
ID   ADD75409 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100714-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 644
ID   ADD76953 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100715-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 645
ID   ADD86721 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100719-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 646
ID   ADD78189 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100731-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 647
ID   ADD77697 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100729-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 648
ID   ADD77943 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100730-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 649
ID   ADD85401 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100725-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 650
ID   ADD73933 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100710-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159;   DB 8;   Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;
RESULT 651
ID   ADD74671 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100713-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.

RESULT 652
ID   ADD77199 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100716-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Pred. No. 6.6e-05;
Best Local Similarity   23.2%;   Score 159; DB 8; Length 352;

RESULT 653
ID   ADD85893 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003100720-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Pred. No. 6.6e-05;
Best Local Similarity   23.2%;   Score 159; DB 8; Length 352;

RESULT 654
ID   ADE05442 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003100723-A1.
PN   US2003100724-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Pred. No. 6.6e-05;
Best Local Similarity   23.2%;   Score 159; DB 8; Length 352;

RESULT 655
ID   ADF74917 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003194760-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Pred. No. 6.6e-05;
Best Local Similarity   23.2%;   Score 159; DB 8; Length 352;

RESULT 656
ID   ADF35631 standard; protein; 352 AA.
DE   Human PRO5723 polypeptide.
PN   US2003228655-A1.
PD   11-DEC-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Pred. No. 6.6e-05;
Best Local Similarity   23.2%;   Score 159; DB 8; Length 352;

RESULT 657
ID   ADG11881 standard; protein; 352 AA.
DE   Human PRO5723 polypeptide.
PN   US2003195959-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Pred. No. 6.6e-05;
Best Local Similarity   23.2%;   Score 159; DB 8; Length 352;

RESULT 658
ID   ADG05729 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003096959-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Pred. No. 6.6e-05;
Best Local Similarity   23.2%;   Score 159; DB 8; Length 352;

RESULT 659
ID   ADG22283 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003096962-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Pred. No. 6.6e-05;
Best Local Similarity   23.2%;   Score 159; DB 8; Length 352;

RESULT 660
ID   ADG11346 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003096967-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Pred. No. 6.6e-05;
Best Local Similarity   23.2%;   Score 159; DB 8; Length 352;

RESULT 661
ID   ADG12125 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003096963-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159; DB 8; Length 352;

RESULT 662
ID   ADF94682 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003096964-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;

RESULT 663
ID   ADG06778 standard; protein; 352 AA.
DE   Human PRO polypeptide #108.
PN   US2003096966-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;

RESULT 664
ID   ADG39122 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2003096965-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;

RESULT 665
ID   ADH19751 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003228656-A1.
PD   11-DEC-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;

RESULT 666
ID   ADH21244 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003224358-A1.
PD   04-DEC-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;

RESULT 667
ID   ADH20284 standard; protein; 352 AA.
DE   Human secreted/transmembrane protein PRO5723.
PN   US2003219856-A1.
PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;

RESULT 668
ID   ADH43713 standard; protein; 352 AA.
DE   Human PRO polypeptide #140.
PN   US2003224984-A1.
PD   04-DEC-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;

RESULT 669
ID   ADG34212 standard; protein; 352 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US2004006206-A1.
PD   08-JAN-2004.
PA   (GETH) GENENTECH INC.
Query Match   7.6%;   Score 159; DB 8; Length 352;
Best Local Similarity   23.2%;   Pred. No. 6.6e-05;

RESULT 670
ID   ADI33682 standard; protein; 352 AA.

DE Human PRO polypeptide #108.
PN US20030096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;

RESULT 672
ID ADH69776 standard; protein; 352 AA.
DE Human PRO polypeptide #108.
PN US20040019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;

RESULT 673
ID ADI29937 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US20030096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;

RESULT 674
ID ADM27334 standard; protein; 352 AA.
DE Human PRO polypeptide #140.
PN US20040043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;

RESULT 675
ID ADK66692 standard; protein; 352 AA.
DE Novel human secreted and transmembrane protein PRO5723.
PN US20040044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 159; DB 8; Length 352;
Best Local Similarity 23.2%; Pred. No. 6.6e-05;

RESULT 676
ID AAW69697 standard; protein; 365 AA.
DE Human coxsackievirus and Ad2 and Ad5 receptor HCAR protein.
PN WO9833819-A1.
PD 06-AUG-1998.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 7.6%; Score 159; DB 2; Length 365;
Best Local Similarity 23.2%; Pred. No. 7e-05;

RESULT 677
ID AAW57212 standard; protein; 365 AA.
DE Human coxsackievirus and adenovirus receptor.
PN WO9811221-A2.
PD 19-MAR-1998.
PA (DAND) DANA FARBER CANCER INST INC.
Query Match 7.6%; Score 159; DB 2; Length 365;
Best Local Similarity 23.2%; Pred. No. 7e-05;

RESULT 678
ID AAB47270 standard; protein; 365 AA.
DE Human CAR.
PN US6245966-B1.
PD 12-JUN-2001.
PA (UYTE-) UNIV TECHNOLOGY CORP.
Query Match 7.6%; Score 159; DB 4; Length 365;
Best Local Similarity 23.2%; Pred. No. 7e-05;

RESULT 679
ID AAB08040 standard; protein; 365 AA.
DE Human coxsackie-adenovirus receptor (CAR).
PN WO200229072-A2.
PD 11-APR-2002.
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
Query Match 7.6%; Score 159; DB 5; Length 365;
Best Local Similarity 23.2%; Pred. No. 7e-05;

RESULT 680
ID AB37063 standard; protein; 365 AA.
DE Human breast cancer / ovarian cancer related protein #39.
PN WO200300012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.6%; Score 159; DB 6; Length 365;
Best Local Similarity 23.2%; Pred. No. 7e-05;

RESULT 681
ID ADB97544 standard; protein; 365 AA.
DE Human CAR wild-type protein.
PN WO200307915-A2.
PD 28-AUG-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 7.6%; Score 159; DB 7; Length 365;
Best Local Similarity 23.2%; Pred. No. 7e-05;

RESULT 682
ID ADN95226 standard; protein; 365 AA.
DE Human BEC/LEC-related protein sequence SeqID148.
PN WO200308640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 7.6%; Score 159; DB 7; Length 365;
Best Local Similarity 23.2%; Pred. No. 7e-05;

RESULT 683
ID ABU12046 standard; protein; 505 AA.
DE Human NOV4a CG59871-01 protein SEQ ID 12.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.6%; Score 159; DB 6; Length 505;
Best Local Similarity 23.2%; Pred. No. 0.00011;

RESULT 684
ID AAY41692 standard; protein; 373 AA.
DE Human PRO 363 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 2; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 685
ID AAB33430 standard; protein; 373 AA.
DE Human PRO363 protein UNQ318 SEQ ID NO:87.
PN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 3; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 686
ID AAB34248 standard; protein; 373 AA.
DE Human PRO363 (UNQ318) protein sequence SEQ ID NO:59.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 3; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 687
ID AAI12365 standard; protein; 373 AA.
DE Human PRO363 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 4; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 688
ID AAB48146 standard; protein; 373 AA.
DE Human coxsackie-adenovirus receptor (CAR).

DE Human A236 variant 2 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match   7.6%; Score 158.5; DB 4; Length 373;
Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 689
ID AAB48108 standard; protein; 373 AA.
DE Human A236 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match   7.6%; Score 158.5; DB 4; Length 373;
Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 690
ID AAB65293 standard; protein; 373 AA.
DE Human PRO363 protein, Seq ID No 130.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 4; Length 373;
Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 691
ID AAU83656 standard; protein; 373 AA.
DE Human PRO protein, Seq ID No 130.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 4; Length 373;
Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 692
ID ABB84848 standard; protein; 373 AA.
DE Human PRO363 protein sequence SEQ ID NO:64.
PN WO200206090-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 5; Length 373;
Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 693
ID AAE26448 standard; protein; 373 AA.
DE Human A236 protein.
PN US20205139-A1.
PD 09-MAY-2002.
PA (HOLT/) HOLTZMAN D A.
PA (SHAR/) SHARP J D.
PA (LEIB/) LEIBY K R.
PA (BOSS/) BOSSONE S.
PA (PANY/) PAN Y.
PA (BARN/) BARNES T M.
PA (FRAS/) FRASER C C.
PA (WRIG/) WRIGHTON N.
PA (MYER/) MYERS P S.
PA (KING/) KINGSBURY G.
Query Match   7.6%; Score 158.5; DB 5; Length 373;
Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 694
ID ABB95454 standard; protein; 373 AA.
DE Human angiogenesis related protein PRO363 SEQ ID NO: 64.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match   7.6%; Score 158.5; DB 5; Length 373;
Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 695
ID ABU58108 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US20030271163-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 5; Length 373;
Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 696
ID ABU59186 standard; protein; 373 AA.
DE Novel human secreted or transmembrane protein PRO363.
PN US20020132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 697
ID ABU82698 standard; protein; 373 AA.
DE Novel human secreted/transmembrane protein PRO363.
PN US20030032023-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 698
ID ABO17809 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 699
ID ABU60617 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, #176.
PN US20021160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 700
ID ABU80803 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US20030036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 701
ID ABO25194 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 702
ID ABO33769 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 703
ID ABU13999 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US20021103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.

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Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 704
ID   ABU81063 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20030043111-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 705
ID   ABU72200 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20030192706-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 706
ID   ABU72584 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20030033531-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 707
ID   ABU66763 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20030036180-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 708
ID   ABU84880 standard; protein; 373 AA.
DE   Human secreted and transmembrane polypeptide PRO363.
PN   US20020177553-A1.
PD   28-NOV-2002.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 709
ID   ABU59844 standard; protein; 373 AA.
DE   Novel secreted and transmembrane protein PRO363.
PN   US20030017563-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 710
ID   ABU61078 standard; protein; 373 AA.
DE   Human PRO363 polypeptide.
PN   US2002169284-A1.
PD   14-NOV-2002;
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 711
ID   ABU59333 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, #176.
PN   US20030027162-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 712
ID   ABO26030 standard; protein; 373 AA.
DE   Human PRO363 polypeptide.
PN   US2002127576-A1.
PD   12-SEP-2002.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;


RESULT 713
ID   ABO25034 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein (PRO) #194.
PN   US20030036179-A1.
PD   20-FEB-2003.
PA   (GETH ) GENENTECH INC.

RESULT 714
ID   ABU80347 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein PRO363.
PN   US20030004102-A1.
PD   02-JAN-2003.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 715
ID   ABU82112 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20030088063-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 716
ID   ABU59039 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, #176.
PN   US20020142961-A1.
PD   03-OCT-2002.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 717
ID   ABU92417 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO5723.
PN   US20030022187-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 718
ID   ABU59482 standard; protein; 373 AA.
DE   Novel human secreted or transmembrane protein PRO5723.
PN   US20030027985-A1.
PD   06-FEB-2003.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 719
ID   ABU67039 standard; protein; 373 AA.
DE   Human secreted/transmembrane, PRO, protein SEQ ID 388.
PN   US20030032155-A1.
PD   13-FEB-2003.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 720
ID   ABU92248 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20030017476-A1.
PD   23-JAN-2003.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 721
ID   ABU10954 standard; protein; 373 AA.
DE   Human PRO polypeptide #140.
PN   US2002123463-A1.
PD   05-SEP-2002.
PA   (GETH ) GENENTECH INC.

Query Match        7.6%;   Score 158.5;  DB 6;  Length 373;
Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 722
ID   ABU81706 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US200217164-A1.
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PD   28-NOV-2002.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 723
ID   ABU88645 standard; protein; 373 AA.
DE   Human secreted and transmembrane polypeptide PRO363.
PN   US2002197615-A1.
PD   26-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 724
ID   ABO34159 standard; protein; 373 AA.
DE   Human PRO363 polypeptide.
PN   US2003017981-A1.
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 725
ID   ADA45907 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003022328-A1.
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 726
ID   ADA76338 standard; protein; 373 AA.
DE   Human PRO363 protein.
PN   US2003073212-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 727
ID   ABJ72292 standard; protein; 373 AA.
DE   Human PRO363 protein.
PN   US2003050448-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 728
ID   ADA18988 standard; protein; 373 AA.
DE   Human PRO363 protein.
PN   US2003054517-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 729
ID   ADA61611 standard; protein; 373 AA.
DE   Homo sapiens.
PN   US2003049816-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 730
ID   ADB19396 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003068796-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 731
ID   ADB27937 standard; protein; 373 AA.
DE   Human PRO363 polypeptide #194.
PN   US2003082704-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.

Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 732
ID   ADA86416 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003082711-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 733
ID   ADB15980 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003087350-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 734
ID   ADA38014 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein PRO363.
PN   US2003008297-A1.
PD   09-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 735
ID   ADA47766 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003073215-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 736
ID   ADA21700 standard; protein; 373 AA.
DE   Human secreted/transmembrane polypeptide PRO363.
PN   US2003054404-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 737
ID   ADA10487 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003068799-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 738
ID   ADA67561 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003068795-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 739
ID   ADB30568 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003068794-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 740
ID   ADA85864 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003082693-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   22.2%;
Best Local Similarity   7.6%;   Score 158.5; DB 6;   Length 373;
RESULT 741

ID ADA18031 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US20030054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 742
ID ADA97076 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 743
ID ADA79380 standard; protein; 373 AA.
DE Human secreted and transmembrane protein PRO363.
PN US20030082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 744
ID ADA87519 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030082745-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 745
ID ADB16721 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 746
ID ADA28139 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US20030082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 747
ID ADA91813 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 748
ID ADB14876 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 749
ID ADA24598 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 750
ID ADB18837 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 751
ID ADA94052 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 752
ID ADB19948 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 753
ID ADB13260 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 754
ID ABO43342 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 755
ID ABO19649 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 756
ID ADA12259 standard; protein; 373 AA.
DE Human secreted/transmembrane polypeptide PRO363.
PN US20030055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 757
ID ADA94719 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US20030059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 758
ID ADA74514 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 759
ID ADB24747 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US20030077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 6; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 760
ID ADA82271 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 761
ID ADA75234 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 762
ID ADA85312 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 763
ID ADA84760 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 764
ID ADA80016 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 765
ID ADA80544 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 766
ID ADA75786 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 767
ID ADA38944 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US20030059780-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 768
ID ADA47011 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 769
ID ADB25307 standard; protein; 373 AA.
DE Human PRO polypeptide SEQ ID NO 388.
PN US20030077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 770
ID ADA93483 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 771
ID ADA26833 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 772
ID ADB31120 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 773
ID ABJ72420 standard; protein; 373 AA.
DE Human PRO363 protein.
PN US20030027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 774
ID ADA93065 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US20030060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 775
ID ADA61048 standard; protein; 373 AA.
DE Homo sapiens.
PN US20030049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 776
ID ADB24195 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 777
ID ADA96524 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%; Score 158.5; DB 6; Length 373;
Query Match 22.2%; Score 158.5; DB 6; Pred. No. 7.9e-05;

RESULT 778
ID ADA81096 standard; protein; 373 AA.

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DE   Human PRO polypeptide #194.
PN   US20030082702-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 6;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 779
ID   ADA95972 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20030082759-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 6;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 780
ID   ADB26281 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20030082760-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 6;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 781
ID   ADB21766 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20030082765-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 6;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 782
ID   ABO34315 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20030044934-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 6;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 783
ID   ABO19540 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane polypeptide PRO 363.
PN   US20030049633-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 6;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 784
ID   ADA77545 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20030068797-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 6;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 785
ID   ADB18285 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20030077710-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 7;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 786
ID   ADA86968 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20030082709-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 7;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 787
ID   ADA88071 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20030082700-A1.

PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 7;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 788
ID   ADA46459 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20030054516-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 7;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 789
ID   ADB28489 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20030082699-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 7;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 790
ID   ADB29041 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20030082706-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 7;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 791
ID   ABO53245 standard; protein; 373 AA.
DE   Novel human secreted/transmembrane protein PRO363.
PN   US20030044806-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 7;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 792
ID   ADA76993 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20030059909-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 7;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 793
ID   ADA22626 standard; protein; 373 AA.
DE   Novel human secreted/transmembrane protein PRO363.
PN   US20030040473-A1.
PD   27-FEB-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 7;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 794
ID   ADA88623 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20030073213-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 7;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 795
ID   ADA97628 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20030082686-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      7.6%;    Score 158.5;  DB 7;  Length 373;
     Best Local Similarity    22.2%;   Pred. No. 7.9e-05;
RESULT 796
ID   ADB27385 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20030022235-A1.
PD   30-JAN-2003.
     Query Match      7.6%;    Score 158.5;  DB 7;  Length 373;
     Best Local Similarity    22.2%;
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RESULT 797
ID   ADB22318 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003087344-A1.
PD   08-MAY-2003.

RESULT 798
ID   ABO22615 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein PRO363.
PN   US2003017982-A1.
PD   23-JAN-2003.

RESULT 799
ID   ADA06792 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein PRO363.
PN   US2003049638-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 800
ID   ABJ72122 standard; protein; 373 AA.
DE   Human membrane bound receptor/protein PRO363 amino acid sequence.
PN   US2003065147-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 801
ID   ADA39485 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein PRO363.
PN   US2003059782-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 802
ID   ADA67009 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003068793-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 803
ID   ADB22870 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003077711-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 804
ID   ADB23643 standard; protein; 373 AA.
DE   Human PRO polypeptide SEQ ID NO 388.
PN   US2003077712-A1.
PD   24-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 805
ID   ADA92365 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003082712-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 806
ID   ADB15428 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003087352-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 807
ID   ADB83620 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003073814-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 808
ID   ADB80726 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003088068-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 809
ID   ADB73267 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003096968-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 810
ID   ADB38680 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003082766-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 811
ID   ADB96511 standard; protein; 373 AA.
DE   Human PRO polypeptide #140.
PN   US2003054403-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 812
ID   ADB78349 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003092889-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 813
ID   ADB38128 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003082689-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 814
ID   ADB66600 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003082689-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
     Query Match   7.6%; Score 158.5; DB 7; Length 373;
     Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 815
ID   ADB84997 standard; protein; 373 AA.
DE   Human PRO polypeptide #65.
PN   US2003073817-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
     Query Match

Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

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RESULT 816
ID   ADB89680 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003082698-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 817
ID   ADB90412 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003082762-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 818
ID   ADB39513 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003082764-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 819
ID   ADB78103 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003092886-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 820
ID   ADB73565 standard; protein; 373 AA.
DE   Human PRO polypeptide #8.
PN   US2003045462-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 821
ID   ADB71169 standard; protein; 373 AA.
DE   Human PRO polypeptide #65.
PN   US2003080667-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 822
ID   ADB84751 standard; protein; 373 AA.
DE   Human PRO polypeptide #65.
PN   US2003092890-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 823
ID   ADB47136 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003082687-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 824
ID   ADB83866 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003069397-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;
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RESULT 825
ID   ADB86743 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003082697-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 826
ID   ADB73021 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003092887-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 827
ID   ADB76281 standard; protein; 373 AA.
DE   Human PRO polypeptide #8.
PN   US2003083248-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 828
ID   ADB77348 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003082696-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 829
ID   ADB84505 standard; protein; 373 AA.
DE   Human PRO polypeptide SEQ ID NO 388.
PN   US2003077717-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 830
ID   ADB35609 standard; protein; 373 AA.
DE   Human PRO polypeptide SEQ ID NO 388.
PN   US2003077719-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 831
ID   ADB33953 standard; protein; 373 AA.
DE   Human PRO polypeptide SEQ ID NO 388.
PN   US2003077716-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 832
ID   ADB35057 standard; protein; 373 AA.
DE   Human PRO polypeptide SEQ ID NO 388.
PN   US2003077718-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 833
ID   ADB36161 standard; protein; 373 AA.
DE   Human PRO polypeptide SEQ ID NO 388.
PN   US2003077720-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
Query Match             7.6%;  Pred. No. 7.9e-05;
Best Local Similarity   22.2%;   Score 158.5; DB 7; Length 373;

RESULT 834
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RESULT 835
ID   ADB46556 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003082692-A1.
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 836
ID   ADC43707 stahdard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US2003054986-A1.
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 837
ID   ADC57983 stahdard; protein; 373 AA.
DE   Human PRO polypeptide #140.
PN   US2003027754-A1.
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 838
ID   ADC55347 stahdard; protein; 373 AA.
DE   Human PRO polypeptide #140.
PN   US2003045463-A1.
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 839
ID   ADC12214 stahdard; protein; 373 AA.
DE   Human secreted/transmembrane protein PRO363.
PN   US2003049681-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 840
ID   ADC61467 stahdard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US2003049684-A1.
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 841
ID   ADC66531 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US2003060406-A1.
PD   27-MAR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 842
ID   ADC56636 standard; protein; 373 AA.
DE   Human PRO polypeptide #140.
PN   US2003064375-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 843
ID   ADC68655 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US2003064407-A1.
PD   03-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 844
ID   ADC62715 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US2003068648-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 845
ID   ADC67780 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US2003069178-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 846
ID   ADC11681 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein PRO363.
PN   US2003069403-A1.
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 847
ID   ADC41100 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US2003072745-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 848
ID   ADC67155 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US2003073131-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 849
ID   ADC62091 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US2003073624-A1.
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 850
ID   ADC36859 standard; protein; 373 AA.
DE   Human PRO polypeptide #65.
PN   US2003088065-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 851
ID   ADC41724 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US2003104998-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 852
ID   ADC21849 standard; protein; 373 AA.
DE   Human PRO polypeptide #65.
PN   US2003096969-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
      Query Match
      Best Local Similarity   22.2%;   Score 158.5;   Pred. No. 7.9e-05;   DB 7;   Length 373;

RESULT 853
ID ADC50429 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 854
ID ADC71976 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 855
ID ADC59955 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 856
ID ADC49980 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 857
ID ADC49079 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 858
ID ADC49596 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 859
ID ADC47457 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 860
ID ADC52962 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 861
ID ADC57316 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 862
ID ADC60507 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 863
ID ADC50982 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 864
ID ADC65509 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 865
ID ADC54607 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 866
ID ADC53568 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 867
ID ADC59091 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 868
ID ADC55969 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 869
ID ADC58539 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 870
ID ADC14803 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein Seq ID388.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;

RESULT 871
ID ADC47202 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.

PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
RESULT 872
ID ADD08335 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
PA (GETH) GENENTECH INC.
RESULT 873
ID ADD03213 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 874
ID ADC90205 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087348-A1.
PD 08-MAY-2003.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
PA (GETH) GENENTECH INC.
RESULT 875
ID ADC82160 standard; protein; 373 AA.
DE Human PRO polypeptide #140.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
PA (GETH) GENENTECH INC.
RESULT 876
ID ADC69624 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194770-A1.
PD 16-OCT-2003.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
PA (GETH) GENENTECH INC.
RESULT 877
ID ADC48513 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194773-A1.
PD 16-OCT-2003.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
PA (GETH) GENENTECH INC.
RESULT 878
ID ADD10042 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194776-A1.
PD 16-OCT-2003.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
PA (GETH) GENENTECH INC.
RESULT 879
ID ADD07802 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2002193299-A1.
PD 19-DEC-2002.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
PA (GETH) GENENTECH INC.
RESULT 880
ID ADC78077 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
RESULT 881
ID ADD04617 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 882
ID ADC82693 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
PA (GETH) GENENTECH INC.
RESULT 883
ID ADD06312 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073816-A1.
PD 17-APR-2003.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
PA (GETH) GENENTECH INC.
RESULT 884
ID ADC80573 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092103-A1.
PD 15-MAY-2003.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
PA (GETH) GENENTECH INC.
RESULT 885
ID ADD11080 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194774-A1.
PD 16-OCT-2003.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
PA (GETH) GENENTECH INC.
RESULT 886
ID ADD10353 standard; protein; 373 AA.
DE Human secreted/transmembrane PRO polypeptide #32.
PN US2003105011-A1.
PD 05-JUN-2003.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
PA (GETH) GENENTECH INC.
RESULT 887
ID ADC47961 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003194771-A1.
PD 16-OCT-2003.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
PA (GETH) GENENTECH INC.
RESULT 888
ID ADD08873 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
PA (GETH) GENENTECH INC.
RESULT 889
ID ADC77831 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003088066-A1.
PD 08-MAY-2003.
Query Match 7.6%; Score 158.5; DB 7; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
PA (GETH) GENENTECH INC.
RESULT 890

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ID   ADC80021 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20030087358-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 891
ID   ADD07122 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2002193300-A1.
PD   19-DEC-2002.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 892
ID   ADD11313 standard; protein; 373 AA.
DE   Human secreted/transmembrane PRO polypeptide #32.
PN   US2003105013-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 893
ID   ADD09490 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003194775-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 894
ID   ADC83369 standard; protein; 373 AA.
DE   Human PRO polypeptide #140.
PN   US2003105291-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 895
ID   ADD50794 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003059783-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 896
ID   ADD41203 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20030203438-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 897
ID   ADD52342 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003194769-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 898
ID   ADD51040 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003105290-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 899
ID   ADD53082 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003194792-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 900
ID   ADD53634 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20030203437-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 901
ID   ADD55476 standard; protein; 373 AA.
DE   Human PRO polypeptide #140.
PN   US20030077593-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 902
ID   ADD37106 standard; protein; 373 AA.
DE   Human secreted/transmembrane PRO polypeptide #32.
PN   US2003105012-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 903
ID   ADD51790 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003194779-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 904
ID   ADD56434 standard; protein; 373 AA.
DE   Human PRO polypeptide #140.
PN   US20030077594-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 905
ID   ADD02589 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20030203431-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 906
ID   ADD50521 standard; protein; 373 AA.
DE   Human PRO polypeptide #65.
PN   US20030096971-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 907
ID   ADD02023 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20030203430-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    7.6%;  Score 158.5;  DB 7;  Length 373;
     Best Local Similarity  22.2%;  Pred. No. 7.9e-05;

RESULT 908
ID   ADD54205 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20030203432-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.
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Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 909
ID   ADD54872 standard; protein; 373 AA.
DE   Human PRO polypeptide #140.
PN   US20021232253-A1.
PD   19-SEP-2002.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 910
ID   ADD50275 standard; protein; 373 AA.
DE   Human PRO polypeptide #65.
PN   US20030966970-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 911
ID   ADD51286 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20031105289-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 912
ID   ADE49093 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US20030967444-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 913
ID   ADD92522 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20031990030-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 914
ID   ADD91418 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20031990055-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 915
ID   ADE04032 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20031990057-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 916
ID   ADE31891 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein PRO363.
PN   US20030068647-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 917
ID   ADE27026 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20030307304-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 918
ID   ADE33433 standard; protein; 373 AA.

ID   ADE32329 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20031947765-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 919
ID   ADE22261 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20031990056-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 920
ID   ADD79485 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20030203428-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 921
ID   ADE35147 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US20030203434-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 922
ID   ADE16261 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US20030203435-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 923
ID   ADD72876 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US20030203436-A1.
PD   30-OCT-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 924
ID   ADE42021 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20031947772-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 925
ID   ADE17838 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20031990023-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 926
ID   ADD91970 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20031990053-A1.
PD   23-OCT-2003.
PA   (GETH ) GENENTECH INC.

Query Match          22.2%;  Score 158.5;  DB 7;  Length 373;
Best Local Similarity 7.6%;  Pred. No. 7.9e-05;
RESULT 927
ID   ADE33433 standard; protein; 373 AA.
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DE   Novel human secreted and transmembrane protein PRO363.
PN   US20031947767-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 928
ID   ADE33985 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003194791-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
PD   06-NOV-2003.
PN   US2003207417-A1.
DE   Human PRO polypeptide #194.
ID   ADD80037 standard; protein; 373 AA.
RESULT 929
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
PA   (GETH) GENENTECH INC.
PD   16-OCT-2003.
PN   US2003194768-A1.
DE   Human PRO polypeptide #194.
ID   ADD93074 standard; protein; 373 AA.
RESULT 930
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
PA   (GETH) GENENTECH INC.
PD   16-OCT-2003.
PN   US2003194781-A1.
DE   Human secreted/transmembrane protein, PRO363.
ID   ADD72234 standard; protein; 373 AA.
RESULT 931
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
PA   (GETH) GENENTECH INC.
PD   23-OCT-2003.
PN   US2003199025-A1.
DE   Human PRO polypeptide #194.
ID   ADE19494 standard; protein; 373 AA.
RESULT 932
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
PA   (GETH) GENENTECH INC.
PD   23-OCT-2003.
PN   US2003199026-A1.
DE   Human PRO polypeptide #194.
ID   ADE18942 standard; protein; 373 AA.
RESULT 933
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
PA   (GETH) GENENTECH INC.
PD   23-OCT-2003.
PN   US2003199033-A1.
DE   Human PRO polypeptide #194.
ID   ADE43138 standard; protein; 373 AA.
RESULT 934
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
PA   (GETH) GENENTECH INC.
PD   23-OCT-2003.
PN   US2003199059-A1.
DE   Human PRO polypeptide #194.
ID   ADD95927 standard; protein; 373 AA.
RESULT 935
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
PA   (GETH) GENENTECH INC.
PD   23-OCT-2003.
PN   US2003199034-A1.
DE   Human PRO polypeptide #194.
ID   ADE22813 standard; protein; 373 AA.
RESULT 936
DE   Human PRO polypeptide #194.

PN   US2003199064-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 937
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
ID   ADD78931 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003203429-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 938
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
ID   ADE26493 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003087305-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
RESULT 939
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
ID   ADE32881 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003194766-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 940
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
ID   ADE42573 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003199032-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 941
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
ID   ADE16885 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US2003203433-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 942
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
ID   ADD80589 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003207418-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
RESULT 943
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
ID   ADD89617 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003199028-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 944
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
ID   ADE40901 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003199031-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
RESULT 945
Best Local Similarity   22.2%;
Query Match   7.6%;   Score 158.5;   DB 7;   Length 373;
     Pred. No. 7.9e-05;
ID   ADE04700 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003199034-A1.
PD   23-OCT-2003.

RESULT 946
ID ADE92829 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20031947777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 947
ID ADF46899 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US20031953333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 948
ID ADF67430 standard; protein; 373 AA.
DE Human PRO363; amino acid sequence SEQ ID NO:503.
PN US20021981148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 949
ID ADG21538 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20032073555-A1.
PD 06-NOV-2003.,
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 950
ID ADG23179 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20032073384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 951
ID ADF97514 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein #194.
PN US20032073770-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 952
ID ADG80578 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20032073773-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 953
ID ADG52656 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US20032165551-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 954
ID ADG59976 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US20032206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 955
ID ADG800026 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20032073772-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 956
ID ADH55318 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20032073381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 957
ID ADH55870 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20032073379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 958
ID ADI35684 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US20032073385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 959
ID ADI60736 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US20032077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 960
ID ADI64089 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20032073386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 961
ID ADI65038 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20032073387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 962
ID ADI63537 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20032073388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 963
ID ADH81951 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20032073388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 22.2%; Score 158.5; DB 7; Pred. No. 7.9e-05;
Best Local Similarity 22.2%; Score 158.5; DB 7; Length 373;

RESULT 964
ID ADI00177 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 7; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 965
ID ADH81199 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 7; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 966
ID ADM82568 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 7; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 967
ID ADN15967 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 7; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 968
ID ADN16596 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 7; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 969
ID ADN15415 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 7; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 970
ID ADN14863 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 7; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 971
ID ADC4833 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 8; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 972
ID ADC81125 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 8; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 973
ID ADE21004 standard; protein; 373 AA.

RESULT 974
ID ADE05848 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 8; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 975
ID ADD76573 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 8; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 976
ID ADD75077 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 8; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 977
ID ADD75823 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 8; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 978
ID ADD85055 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 8; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 979
ID ADD86881 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 8; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 980
ID ADB20758 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 8; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 981
ID ADB39055 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
  Query Match   7.6%; Score 158.5; DB 8; Length 373;
  Best Local Similarity   22.2%; Pred. No. 7.9e-05;

RESULT 982
ID ADB87937 standard; protein; 373 AA.
DE Human PRO polypeptide #194.

PN US20030092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 983
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADD86341 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20032034440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

RESULT 984
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADE05602 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US20031007227-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

RESULT 985
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADD73587 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US20031007211-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

RESULT 986
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADE75789 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20031211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.

RESULT 987
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADE48393 standard; protein; 373 AA.
DE Novel human secreted/transmembrane protein, PRO363.
PN US20031104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

RESULT 988
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADD78427 standard; protein; 373 AA.
DE Novel human secreted and transmembrane PRO polypeptide #32.
PN US20031000737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

RESULT 989
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADD41314 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US20031000497-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

RESULT 990
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADE23365 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

RESULT 991
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADE21250 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20031000736-A1.

PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 992
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADD77365 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20031000732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

RESULT 993
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADE20512 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20031000733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

RESULT 994
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADD75577 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US20031000064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

RESULT 995
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADD74093 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US20031000708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

RESULT 996
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADD74339 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US20031000709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

RESULT 997
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADD76069 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20031000718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

RESULT 998
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADD85561 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20031000721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

RESULT 999
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADE23917 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.

RESULT 1000
Query Match 7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity 22.2%; Pred. No. 7.9e-05;
ID ADE24560 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030092111-A1.
PD 15-MAY-2003.

RESULT 1001
ID   ADD87385 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003203439-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity   22.2%;
                        Pred. No. 7.9e-05;

RESULT 1002
ID   ADE05110 standard; protein; 373 AA.
DE   Human PRO polypeptide #65.
PN   US2003100726-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity   22.2%;
                        Pred. No. 7.9e-05;

RESULT 1003
ID   ADD75323 standard; protein; 373 AA.
DE   Human PRO polypeptide #65.
PN   US2003100714-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity   22.2%;
                        Pred. No. 7.9e-05;

RESULT 1004
ID   ADD76867 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003100715-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity   22.2%;
                        Pred. No. 7.9e-05;

RESULT 1005
ID   ADD86635 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003100719-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity   22.2%;
                        Pred. No. 7.9e-05;

RESULT 1006
ID   ADD89251 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003199062-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity   22.2%;
                        Pred. No. 7.9e-05;

RESULT 1007
ID   ADD78103 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003100731-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity   22.2%;
                        Pred. No. 7.9e-05;

RESULT 1008
ID   ADE18390 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003194794-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity   22.2%;
                        Pred. No. 7.9e-05;

RESULT 1009
ID   ADE88699 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003199054-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.

RESULT 1010
ID   ADB89494 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US2003130181-A1.
PD   10-JUL-2003.
PA   (ASHK/) ASHKENAZI A J.
PA   (BAKE/) BAKER K P.
PA   (BOTS/) BOTSTEIN D.
PA   (DESN/) DESNOYERS L.
PA   (EATO/) EATON D L.
PA   (FERR/) FERRARA N.
PA   (FILV/) FILVAROFF E.
PA   (FONG/) FONG S.
PA   (GAO/) GAO W.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GIRM/) GIRMALDI J C.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (KLJA/) KLJAVIN I J.
PA   (KUOS/) KUO S S.
PA   (NAPI/) NAPIER M A.
PA   (PANJ/) PAN J.
PA   (PAON/) PAONI N F.
PA   (ROYM/) ROY M A.
PA   (SHEL/) SHELTON D L.
PA   (STEW/) STEWART T A.
PA   (TUMA/) TUMAS D.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Query Match   7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity   22.2%;
                        Pred. No. 7.9e-05;

RESULT 1011
ID   ADD77611 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003100729-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity   22.2%;
                        Pred. No. 7.9e-05;

RESULT 1012
ID   ADD77857 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003100730-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity   22.2%;
                        Pred. No. 7.9e-05;

RESULT 1013
ID   ADB85315 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003100725-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity   22.2%;
                        Pred. No. 7.9e-05;

RESULT 1014
ID   ADD73847 standard; protein; 373 AA.
DE   Human PRO polypeptide #65.
PN   US2003100710-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8; Length 373;
Best Local Similarity   22.2%;
                        Pred. No. 7.9e-05;

RESULT 1015
ID   ADD74585 standard; protein; 373 AA.
DE   Human PRO polypeptide #65.
PN   US2003100713-A1.
PD   29-MAY-2003.
PA   (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
PD 29-MAY-2003.
PN US2003100716-A1.
DE Novel human secreted and transmembrane protein PRO363.
ID ADD77113 standard; protein; 373 AA.
RESULT 1016
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

PA (GETH) GENENTECH INC.
PD 29-MAY-2003.
PN US2003100720-A1.
DE Novel human secreted and transmembrane protein PRO363.
ID ADD85807 standard; protein; 373 AA.
RESULT 1017
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

PA (GETH) GENENTECH INC.
PD 29-MAY-2003.
PN US2003100723-A1.
DE Human PRO polypeptide #65.
ID ADD74831 standard; protein; 373 AA.
RESULT 1018
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

PA (GETH) GENENTECH INC.
PD 29-MAY-2003.
PN US2003100724-A1.
DE Human PRO polypeptide #65.
ID ADE05356 standard; protein; 373 AA.
RESULT 1019
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

PA (GETH) GENENTECH INC.
PD 16-OCT-2003.
PN US2003195345-A1.
DE Human secreted/transmembrane protein, PRO363.
ID ADF61134 standard; protein; 373 AA.
RESULT 1020
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

PA (GETH) GENENTECH INC.
PD 16-OCT-2003.
PN US2003198994-A1.
DE Human secreted/transmembrane protein, PRO363.
ID ADF39826 standard; protein; 373 AA.
RESULT 1021
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

PA (GETH) GENENTECH INC.
PD 16-OCT-2003.
PN US2003195148-A1.
DE Human secreted/transmembrane protein, PRO363.
ID ADF45622 standard; protein; 373 AA.
RESULT 1022
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

PA (GETH) GENENTECH INC.
PD 23-OCT-2003.
PN US2003199027-A1.
DE Human PRO polypeptide #194.
ID ADE94719 standard; protein; 373 AA.
RESULT 1023
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

PA (GETH) GENENTECH INC.
PD 23-OCT-2003.
PN US2003199061-A1.
DE Human PRO polypeptide #194.
ID ADE91130 standard; protein; 373 AA.
RESULT 1024
Best Local Similarity 22.2%;

Query Match 7.6%;   Pred. No. 7.9e-05;
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
RESULT 1025
ID ADF35629 standard; protein; 373 AA.
DE Human PRO363 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 7.6%;   Pred. No. 7.9e-05;
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
RESULT 1026
ID ADD95271 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 7.6%;   Pred. No. 7.9e-05;
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
RESULT 1027
ID ADE93381 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 7.6%;   Pred. No. 7.9e-05;
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
RESULT 1028
ID ADF24018 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003204055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 7.6%;   Pred. No. 7.9e-05;
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
RESULT 1029
ID ADF40450 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 7.6%;   Pred. No. 7.9e-05;
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
RESULT 1030
ID ADF23394 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 7.6%;   Pred. No. 7.9e-05;
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
RESULT 1031
ID ADF33377 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 7.6%;   Pred. No. 7.9e-05;
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
RESULT 1032
ID ADF34962 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 7.6%;   Pred. No. 7.9e-05;
Best Local Similarity 22.2%;   Score 158.5;   DB 8;   Length 373;
RESULT 1033
ID ADF26844 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;

RESULT 1034
ID   ADP27480 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein; PRO363.
PN   US2003199437-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1035
ID   ADE92277 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003199051-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1036
ID   ADE90578 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003199063-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1037
ID   ADF41074 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein; PRO363.
PN   US2003199435-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1038
ID   ADF32753 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US2003211091-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1039
ID   ADF25119 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US2003211092-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1040
ID   ADF26220 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US2003199674-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1041
ID   ADF34009 standard; protein; 373 AA.
DE   Human PRO polypeptide, PRO363.
PN   US2003194410-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1042
ID   ADF46246 standard; protein; 373 AA.
DE   Human secreted and transmembrane protein PRO363.
PN   US2003195344-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1043
ID   ADF98637 standard; protein; 373 AA.

RESULT 1044
ID   ADE91725 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003199058-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1045
ID   ADG11879 standard; protein; 373 AA.
DE   Human PRO363 polypeptide.
PN   US2003228655-A1.
PD   11-DEC-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1046
ID   ADG05643 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003096959-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1047
ID   ADG27197 standard; protein; 373 AA.
DE   Human PRO polypeptide #65.
PN   US2003096962-A1.
PD   22-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1048
ID   ADG02304 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003207352-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1049
ID   ADG22090 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003207360-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1050
ID   ADG20160 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003207376-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1051
ID   ADF98066 standard; protein; 373 AA.
DE   Human PRO polypeptide.
PN   US2003207422-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

RESULT 1052
ID   ADG24283 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003207426-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match   7.6%; Score 158.5; DB 8;
Best Local Similarity   22.2%; Pred. No. 7.9e-05; Length 373;

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DE   Human PRO polypeptide #194.
PN   US2003208055-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
RESULT 1053
ID   ADG03468 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003207351-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1054
ID   ADF99189 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003207359-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1055
ID   ADG16774 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003207375-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1056
ID   ADG05233 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003207374-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1057
ID   ADG19500 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003207425-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1058
ID   ADG11260 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003096967-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1059
ID   ADG11337 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003207357-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1060
ID   ADG08394 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003207424-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1061
ID   ADG15564 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.


PN   US2003219885-A1.
PD   27-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1062
ID   ADG12039 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003096963-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1063
ID   ADF96962 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003207371-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1064
ID   ADG06147 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003207389-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1065
ID   ADG23731 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003207423-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1066
ID   ADG04020 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US2003207427-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1067
ID   ADG24921 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003207427-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1068
ID   ADF94596 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003096964-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1069
ID   ADG07218 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003207350-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         7.6%;   Score 158.5;   DB 8;   Length 373;
     Best Local Similarity   22.2%;   Pred. No. 7.9e-05;

RESULT 1070
ID   ADG07770 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US2003207356-A1.
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PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;   Score 158.5;   Length 373;
RESULT 1071
ID ADG06692 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US20030969966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1072
ID ADG55265 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1073
ID ADG60929 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1074
ID ADG62033 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1075
ID ADG82234 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1076
ID ADG57473 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1077
ID ADG56921 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1078
ID ADG55817 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1079
ID ADG58577 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030207368-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1080
ID ADG70943 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1081
ID ADH39036 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1082
ID ADG58025 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1083
ID ADG53609 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1084
ID ADG71495 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1085
ID ADG50232 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US20030207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1086
ID ADG81682 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1087
ID ADH19749 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US20030228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;
Best Local Similarity 22.2%;   Pred. No. 7.9e-05;   Length 373;
RESULT 1088
ID ADH30644 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.6%;   Score 158.5;   DB 8;   Length 373;

RESULT 1089
ID   ADH12011 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20003207419-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1090
ID   ADG49608 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US20003215905-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1091
ID   ADG51480 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US20003215908-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1092
ID   ADG52433 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20003207414-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1093
ID   ADG54161 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20003207416-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1094
ID   ADG48984 standard; protein; 373 AA.
DE   Human secreted and transmembrane protein, PRO363.
PN   US20003216305-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1095
ID   ADG81130 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20003194793-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1096
ID   ADG56369 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20003207366-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1097
ID   ADH12635 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20003207378-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1098
ID   ADG48360 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US20003216560-A1.
PD   20-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1099
ID   ADH21242 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20003207429-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1100
ID   ADG61481 standard; protein; 373 AA.
DE   Human secreted and transmembrane protein PRO363.
PN   US20003219856-A1.
PD   27-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1101
ID   ADH20282 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
PN   US20003022331-A1.
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1102
ID   ADH28568 standard; protein; 373 AA.
DE   Human PRO polypeptide #194.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1103
ID   ADG54713 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20003207367-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1104
ID   ADG59753 standard; protein; 373 AA.
DE   Novel human secreted and transmembrane protein PRO363.
PN   US20003207369-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1105
ID   ADG50856 standard; protein; 373 AA.
DE   Human secreted/transmembrane protein, PRO363.
PN   US20004005312-A1.
PD   08-JAN-2004.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1106
ID   ADH43497 standard; protein; 373 AA.
DE   Human PRO polypeptide #32.
PN   US20003224984-A1.
PD   04-DEC-2003.
PA   (GETH) GENENTECH INC.
Query Match 7.6%;
Best Local Similarity 22.2%;
Score 158.5; Pred. No. 7.9e-05; DB 8; Length 373;

RESULT 1107
ID   ADG58800 standard; protein; 373 AA.

DE Human secreted/transmembrane protein, PRO363.
PN US20040005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1108
ID ADG34126 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20040006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1109
ID ADG62256 standard; protein; 373 AA.
DE Human secreted/transmembrane protein PRO363.
PN US20040006219-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1110
ID ADI81177 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1111
ID ADI33596 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US20030096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1112
ID ADH69690 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US20040019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1113
ID ADH25281 standard; protein; 373 AA.
DE Human neurotrimin homologue related protein sequence SEQ ID NO:59.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1114
ID ADG09920 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20040009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1115
ID ADI15391 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1116
ID ADG09268 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.

PN US20040009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1117
ID ADI14723 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1118
ID ADI29851 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1119
ID ADI18318 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20040044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1120
ID ADM27248 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20040039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1121
ID ADG63599 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20040038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1122
ID AD77494 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20040038336-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1123
ID ADK82842 standard; protein; 373 AA.
DE Human PRO polypeptide #32.
PN US20040043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1124
ID ADK66606 standard; protein; 373 AA.
DE Human PRO polypeptide #65.
PN US20040044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Best Local Similarity 22.2%;   Score 158.5; DB 8; Length 373;
Query Match 7.6%;   Pred. No. 7.9e-05;

RESULT 1125
ID ADG65616 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20040038335-A1.

PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match   22.2%; Score 158.5; DB 8; Length 373;
Best Local Similarity 7.6%; Pred. No. 7.9e-05;
RESULT 1126
ID ADM27752 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20040048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match   22.2%; Score 158.5; DB 8; Length 373;
Best Local Similarity 7.6%; Pred. No. 7.9e-05;
RESULT 1127
ID ADM17058 standard; protein; 373 AA.
DE Human secreted/transmembrane protein, PRO363.
PN US20040048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match   22.2%; Score 158.5; DB 8; Length 373;
Best Local Similarity 7.6%; Pred. No. 7.9e-05;
RESULT 1128
ID ADL06892 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20040063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match   22.2%; Score 158.5; DB 8; Length 373;
Best Local Similarity 7.6%; Pred. No. 7.9e-05;
RESULT 1129
ID ADM42476 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20040058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match   22.2%; Score 158.5; DB 8; Length 373;
Best Local Similarity 7.6%; Pred. No. 7.9e-05;
RESULT 1130
ID ADN05373 standard; protein; 373 AA.
DE Antipsoriatic protein sequence #858.
PN WO200402879-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match   22.2%; Score 158.5; DB 8; Length 373;
Best Local Similarity 7.6%; Pred. No. 7.9e-05;
RESULT 1131
ID ADM28338 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20040077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match   22.2%; Score 158.5; DB 8; Length 373;
Best Local Similarity 7.6%; Pred. No. 7.9e-05;
RESULT 1132
ID ADO36720 standard; protein; 373 AA.
DE Human UKW polypeptide, SEQ ID NO:2.
PN EP1416279-A1.
PD 06-MAY-2004.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match   22.2%; Score 158.5; DB 8; Length 373;
Best Local Similarity 7.6%; Pred. No. 7.9e-05;
RESULT 1133
ID ADI95820 standard; protein; 373 AA.
DE Human PRO polypeptide #194.
PN US20030077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match   22.2%; Score 158.5; DB 8; Length 373;
Best Local Similarity 7.6%; Pred. No. 7.9e-05;
RESULT 1134
ID ADI96372 standard; protein; 373 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US20030207354-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match   22.2%; Score 158.5; DB 8; Length 373;
Best Local Similarity 7.6%; Pred. No. 7.9e-05;
RESULT 1135
ID ADA50171 standard; protein; 412 AA.
DE Human CAR/mouse SCF fusion protein.
PN US20030092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match   24.8%; Score 158.5; DB 6; Length 412;
Best Local Similarity 7.6%; Pred. No. 9.2e-05;
RESULT 1136
ID AD267617 standard; protein; 351 AA.
DE Human ovarian specific polypeptide SEQ ID NO:331.
PN WO200401311-A2.
PD 12-FEB-2004.
PA (DIAD/) DIADEXUS INC.
Query Match   23.0%; Score 157.5; DB 8; Length 351;
Best Local Similarity 7.5%; Pred. No. 8.9e-05;
RESULT 1137
ID ADA50172 standard; protein; 493 AA.
DE Human CAR/mouse anti-CD34 antibody fusion protein.
PN US20030092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match   23.7%; Score 157.5; DB 6; Length 493;
Best Local Similarity 7.5%; Pred. No. 0.00014;
RESULT 1138
ID AAW82729 standard; protein; 264 AA.
DE Adenovirus pACTSG2-SCAR protein.
PN WO9854346-A1.
PD 03-DEC-1998.
PA (GENV-) GENVEC INC.
Query Match   25.9%; Score 156.5; DB 2; Length 264;
Best Local Similarity 7.5%; Pred. No. 7.2e-05;
RESULT 1139
ID AAW82730 standard; protein; 277 AA.
DE Adenovirus SCAR.RGD protein.
PN WO9854346-A1.
PD 03-DEC-1998.
PA (GENV-) GENVEC INC.
Query Match   25.9%; Score 156.5; DB 2; Length 277;
Best Local Similarity 7.5%; Pred. No. 7.7e-05;
RESULT 1140
ID AAU83699 standard; protein; 290 AA.
DE Human PRO protein, Seq ID No 216.
PN WO2002028288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match   25.9%; Score 156.5; DB 5; Length 290;
Best Local Similarity 7.5%; Pred. No. 8.3e-05;
RESULT 1141
ID AAB48145 standard; protein; 373 AA.
DE Human A236 variant 1 polypeptide.
PN WO2000059885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match   22.2%; Score 156.5; DB 4; Length 373;
Best Local Similarity 7.5%; Pred. No. 0.00012;
RESULT 1142
ID AAW82731 standard; protein; 397 AA.
DE Adenovirus pACSG25CAR.sig chimeric protein.
PN WO9854346-A1.
PD 03-DEC-1998.
PA (GENV-) GENVEC INC.
Query Match   25.9%; Score 156.5; DB 2; Length 397;
Best Local Similarity 7.5%; Pred. No. 0.00013;

RESULT 1143
ID   ADA50170 standard; protein; 412 AA.
DE   Human CAR/SCF fusion protein.
PN   US2003092068-A1.
PD   15-MAY-2003.
PA   (ITOH/) ITOH A.
PA   (HANA/) HANAZONO Y.
PA   (OKAD/) OKADA T.
PA   (OZAW/) OZAWA K.
     Query Match   7.5%;
     Best Local Similarity 25.9%; Score 156.5; DB 6; Length 412;

RESULT 1144
ID   ABG02019 standard; protein; 737 AA.
DE   Novel human diagnostic protein #2010.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.
     Query Match   7.4%;
     Best Local Similarity 24.3%; Score 156; DB 4; Length 737;

RESULT 1145
ID   AAB48147 standard; protein; 373 AA.
DE   Human A236 variant 3 polypeptide.
PN   WO200069885-A2.
PD   23-NOV-2000.
PA   (MILL-) MILLENNIUM PHARM INC.
     Query Match   7.4%;
     Best Local Similarity 22.0%; Score 155.5; DB 4; Length 373;

RESULT 1146
ID   ADR66297 standard; protein; 358 AA.
DE   Human prostatic carcinoma derived protein SEQ ID 151 #2.
PN   WO200076614-A2.
PD   10-SEP-2004.
PA   (HINZ/) HINZMANN B.
PA   (DAHL/) DAHL E.
PA   (ROSE/) ROSENTHAL A.
PA   (HERM/) HERMANN K.
PA   (PILA/) PILARSKY C.
     Query Match   7.4%;
     Best Local Similarity 23.1%; Score 156; DB 4; Length 358;

RESULT 1147
ID   ADR66658 standard; protein; 358 AA.
DE   Human prostatic carcinoma derived DNA SEQ ID 151 #4.
PN   WO200076614-A2.
PD   10-SEP-2004.
PA   (HINZ/) HINZMANN B.
PA   (DAHL/) DAHL E.
PA   (ROSE/) ROSENTHAL A.
PA   (HERM/) HERMANN K.
PA   (PILA/) PILARSKY C.
     Query Match   7.4%;
     Best Local Similarity 23.1%; Score 154.5; DB 8; Length 358;

RESULT 1148
ID   ADA54925 standard; protein; 512 AA.
DE   Human protein, SEQ ID 2493.
PN   EP1293569-A2.
PD   19-MAR-2003.
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
     Query Match   7.4%;
     Best Local Similarity 23.1%; Score 154.5; DB 8; Length 512;

RESULT 1149
ID   ABP60991 standard; protein; 5635 AA.
DE   Novel human protein, SEQ ID 78.
PN   WO200250105-A1.
PD   27-JUN-2002.
PA   (SMIK) SMITHKLINE BEECHAM CORP.
PA   (SMIK) SMITHKLINE BEECHAM PLC.
PA   (GLAX) GLAXO GROUP LTD.
     Query Match   7.4%;
     Best Local Similarity 23.8%; Score 154.5; DB 5; Length 5635;

RESULT 1150
ID   ADJ70089 standard; protein; 5636 AA.
DE   Human heat mitochondrial protein as a therapeutic target SeqID1895.
PN   WO2003087768-A2.
PD/ 23-OCT-2003.
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
     Query Match   7.4%;
     Best Local Similarity 23.4%; Score 154.5; DB 7; Length 5636;

RESULT 1151
ID   ADJ83137 standard; protein; 5636 AA.
DE   Human hemicentin protein - SEQ ID 128.
PN   US2003170630-A1.
PD   11-SEP-2003.
PA   (ALSO/) ALSOBROOK J P.
PA   (TCHE/) TCHERNEV V T.
PA   (LIUX/) LIU X.
PA   (SPYT/) SPYTEK K A.
PA   (ZERH/) ZERHUSEN B D.
PA   (PATT/) PATTURAJAN M.
PA   (LEPL/) LEPLEY D M.
PA   (BURG/) BURGESS C E.
PA   (SHIM/) SHIMKETS R A.
PA   (GROS/) GROSSE W M.
PA   (SZEK/) SZEKERES E S.
PA   (VERN/) VERNET C A M.
PA   (LILL/) LI L.
PA   (CASM/) CASMAN S J.
PA   (BOLD/) BOLDOG F L.
PA   (GORM/) GORMAN L.
PA   (GANG/) GANGOLLI E A.
PA   (FERN/) FERNANDES E R.
PA   (RIEG/) RIEGER D K.
PA   (EDIN/) EDINGER S R.
PA   (GUNT/) GUNTHER E.
PA   (MILL/) MILLET I.
PA   (SCIO/) SCIORE P.
PA   (ELLE/) ELLERMAN K.
PA   (MACD/) MACDOUGALL J R.
PA   (SMIT/) SMITHSON G.
     Query Match   7.4%;
     Best Local Similarity 23.4%; Score 154.5; DB 8; Length 5636;

RESULT 1152
ID   ADK60205 standard; protein; 5636 AA.
DE   Angiogenesis differentially expressed protein GS-P29.
PN   FR2836687-A1.
PD   05-SEP-2003.
PA   (GENE-) GENE SIGNAL.
PA   (ALMA/) AL MAHMOOD S.
     Query Match   7.4%;
     Best Local Similarity 23.4%; Score 154.5; DB 8; Length 5636;

RESULT 1153
ID   ADK60506 standard; protein; 5636 AA.
DE   Angiogenesis differentially expressed protein GS-P29.
PN   FR2836686-A1.
PD   05-SEP-2003.
PA   (GENE-) GENE SIGNAL.
PA   (ALMA/) AL MAHMOOD S.
     Query Match   7.4%;
     Best Local Similarity 23.4%; Score 154.5; DB 8; Length 5636;

RESULT 1154
ID   ADP73129 standard; protein; 5636 AA.
DE   Angiogenesis inhibitor human protein sequence, GS-P29.
PN   FR2843753-A1.
PD   27-FEB-2004.
PA   (GENE/) GENE S.
PA   (ALMS/) ALM S.
     Query Match   7.4%;
     Best Local Similarity 23.4%; Score 154.5; DB 8; Length 5636;

RESULT 1155
ID   AAY53666 standard; protein; 4412 AA.
DE   Sequence gi/1017427/emb/CAA62189 from an alignment with protein 608.
PN   WO9960164-A1.
PD   25-NOV-1999.
PA   (QUAR-) QUARK BIOTECH INC.
     Query Match   7.3%;
     Best Local Similarity   ...; Score 153.5; DB 3; Length 4412;

Best Local Similarity   22.0%; Pred. No. 0.0074;

RESULT 1156
ID ADA50158 standard; protein; 393 AA.
DE Human CAR/mouse SCF mature fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match   7.3%;   Score 153; DB 6; Length 393;
Best Local Similarity   24.3%; Pred. No. 0.00026;

RESULT 1157
ID ADA50159 standard; protein; 474 AA.
DE Human CAR/mouse anti-CD34 antibody mature fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match   7.2%;   Score 152; DB 6; Length 474;
Best Local Similarity   23.2%; Pred. No. 0.00041;

RESULT 1158
ID AAU17996 standard; protein; 301 AA.
DE Human immunoglobulin polypeptide SEQ ID No 141.
PD 02-AUG-2001.
PN WO200155315-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match   7.2%;   Score 151; DB 4; Length 301;
Best Local Similarity   25.8%; Pred. No. 0.00026;

RESULT 1159
ID ABB10232 standard; protein; 301 AA.
DE Human cDNA SEQ ID NO: 540.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match   7.2%;   Score 151; DB 4; Length 301;
Best Local Similarity   25.8%; Pred. No. 0.00026;

RESULT 1160
ID ABP66819 standard; protein; 301 AA.
DE Human polypeptide SEQ ID NO 540.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match   7.2%;   Score 151; DB 5; Length 301;
Best Local Similarity   25.8%; Pred. No. 0.00026;

RESULT 1161
ID ADB31620 standard; protein; 301 AA.
DE Human novel protein SEQ ID NO 141.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match   7.2%;   Score 151; DB 7; Length 301;
Best Local Similarity   25.8%; Pred. No. 0.0026;

RESULT 1162
ID ADR41522 standard; protein; 318 AA.
DE Human CD-like molecule HKAC103, SEQ ID NO:321.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match   7.2%;   Score 151; DB 5; Length 318;
Best Local Similarity   25.8%; Pred. No. 0.00028;

RESULT 1163
ID ADA50157 standard; protein; 393 AA.
DE Human CAR/SCF mature fusion protein.
PN US2003092068-A1.
PD 15-MAY-2003.
PA (ITOH/) ITOH A.
PA (HANA/) HANAZONO Y.
PA (OKAD/) OKADA T.
PA (OZAW/) OZAWA K.
Query Match   7.2%;   Score 151; DB 6; Length 393;
Best Local Similarity   25.4%; Pred. No. 0.00038;

RESULT 1164
ID ABG02117 standard; protein; 434 AA.
DE Novel human diagnostic protein #2108.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match   7.2%;   Score 151; DB 6; Length 434;
Best Local Similarity   24.3%; Pred. No. 0.00044;

RESULT 1165
ID ABU62399 standard; protein; 466 AA.
DE Chimeric CAR/Hg/Pro-A gene product.
PN US6524572-B1.
PD 25-FEB-2003.
PA (RAIN-) RAINBOW THERAPEUTIC CO.
Query Match   7.2%;   Score 151; DB 6; Length 466;
Best Local Similarity   25.4%; Pred. No. 0.00049;

RESULT 1166
ID AAY08401 standard; protein; 1395 AA.
DE Drosophila sp. ROBO1 protein.
PN WO9920764-A1.
PD 29-APR-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match   7.2%;   Score 150; DB 7; Length 1395;
Best Local Similarity   20.5%; Pred. No. 0.0028;

RESULT 1167
ID AAV13563 standard; protein; 1395 AA.
DE Drosophila Robo 1 polypeptide.
PN WO9925833-A1.
PD 27-MAY-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match   7.1%;   Score 150; DB 2; Length 1395;
Best Local Similarity   20.5%; Pred. No. 0.0028;

RESULT 1168
ID ADB85335 standard; protein; 1395 AA.
DE Fruitfly nerve cell growth modulator SLIT-1-associated sequence #1.
PN US2003170727-A1.
PD 11-SEP-2003.
PA (GOOD/) GOODMAN C S.
PA (KIDD/) KIDD T.
PA (BROS/) BROSE K.
PA (TESS/) TESSIER-LAVIGNE M.
Query Match   7.1%;   Score 150; DB 7; Length 1395;
Best Local Similarity   20.5%; Pred. No. 0.0028;

RESULT 1169
ID AAB85862 standard; protein; 373 AA.
DE Murine adipocytes-derived protein.
PN WO200166720-A1.
PD 13-SEP-2001.
PA (KITA/) KITAMURA T.
PA (TSUR/) TSURUGA H.
Query Match   7.1%;   Score 149; DB 4; Length 373;
Best Local Similarity   20.5%; Pred. No. 0.0035;

RESULT 1170
ID ABB68257 standard; protein; 1395 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 31563.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match   7.1%;   Score 149; DB 4; Length 1395;
Best Local Similarity   21.7%; Pred. No. 0.0053;

RESULT 1171
ID AAB48126 standard; protein; 373 AA.
DE Mouse A236 polypeptide.
PN WO200069885-A2.
PD 23-NOV-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match   7.1%;   Score 148; DB 4; Length 373;
Best Local Similarity   21.7%; Pred. No. 0.00064;

RESULT 1172
ID AAE26449 standard; protein; 373 AA.

DE   Mouse A236 protein.
PN   US20020205139-A1.
PD   09-MAY-2002.
PA   (HOLT/) HOLTZMAN D A.
PA   (SHAR/) SHARP J D.
PA   (LEIB/) LEIBY K R.
PA   (BOSS/) BOSSONE S.
PA   (PANY/) PAN Y.
PA   (BARN/) BARNES T M.
PA   (FRAS/) FRASER C C.
PA   (WRIG/) WRIGHTON N.
PA   (MYER/) MYERS P S.
PA   (KING/) KINGSBURY G.

  Query Match
  Best Local Similarity 21.7%; Score 148; DB 5; Length 373;
  Pred. No. 0.00064;
RESULT 1173

ID   ABG31321 standard; protein; 2652 AA.
DE   Predicted human adlican-2 protein.
PN   US2004246364-A2.
PD   13-JUN-2002.
PA   (QUAR-) QUARK BIOTECH INC.

  Query Match
  Best Local Similarity 21.8%; Score 147.5; DB 5; Length 2652;
  Pred. No. 0.012;
RESULT 1174

ID   ADL02250 standard; protein; 2652 AA.
DE   Human OCP protein #6.
PN   US2004053301-A1.
PD   18-MAR-2004.
PA   (QUAR-) QUARK BIOTECH INC.

  Query Match
  Best Local Similarity 21.8%; Score 147.5; DB 8; Length 2652;
  Pred. No. 0.012;
RESULT 1175

ID   ABP70049 standard; protein; 2845 AA.
DE   Human NOV1a.
PN   WO200272771-A2.
PD   19-SEP-2002.
PA   (CURA-) CURAGEN CORP.

  Query Match
  Best Local Similarity 21.8%; Score 147.5; DB 5; Length 2845;
  Pred. No. 0.013;
RESULT 1176

ID   AAB48149 standard; protein; 373 AA.
DE   Mouse A236 variant 2 polypeptide.
PN   WO200069885-A2.
PD   23-NOV-2000.
PA   (MILL-) MILLENNIUM PHARM INC.

  Query Match
  Best Local Similarity 21.7%; Score 147; DB 4; Length 373;
  Pred. No. 0.012;
RESULT 1177

ID   AAB48150 standard; protein; 373 AA.
DE   Mouse A236 variant 3 polypeptide.
PN   WO200069885-A2.
PD   23-NOV-2000.
PA   (MILL-) MILLENNIUM PHARM INC.

  Query Match
  Best Local Similarity 21.7%; Score 147; DB 4; Length 373;
  Pred. No. 0.0078;
RESULT 1178

ID   AAB48148 standard; protein; 373 AA.
DE   Mouse A236 variant 1 polypeptide.
PN   WO200069885-A2.
PD   23-NOV-2000.
PA   (MILL-) MILLENNIUM PHARM INC.

  Query Match
  Best Local Similarity 21.7%; Score 147; DB 4; Length 373;
  Pred. No. 0.0078;
RESULT 1179

ID   ABG22401 standard; protein; 361 AA.
DE   Novel human diagnostic protein #2392.
PN   WO200175067-A2.
PD   11-OCT-2001.
PA   (HYSE-) HYSEQ INC.

  Query Match
  Best Local Similarity 24.5%; Score 146.5; DB 4; Length 361;
  Pred. No. 0.0083;
RESULT 1180

ID   ABB66424 standard; protein; 2016 AA.

DE   Drosophila melanogaster polypeptide SEQ ID NO 26064.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.

  Query Match
  Best Local Similarity 22.1%; Score 145.5; DB 4; Length 2016;
  Pred. No. 0.012;
RESULT 1181

ID   ABB64120 standard; protein; 1033 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 19152.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.

  Query Match
  Best Local Similarity 20.9%; Score 144.5; DB 8; Length 1033;
  Pred. No. 0.0055;
RESULT 1182

ID   ADQ89652 standard; protein; 367 AA.
DE   Antagonist of cell cycle progression polypeptide #41.
PN   WO2004063362-A2.
PD   29-JUL-2004.
PA   (CYCL-) CYCLACEL LTD.

  Query Match
  Best Local Similarity 20.9%; Score 144.5; DB 4; Length 1033;
  Pred. No. 0.0021;
RESULT 1183

ID   ADG63213 standard; protein; 367 AA.
DE   Human neurotrimin protein +69bp isoform.
PN   WO2003002765-A2.
PD   09-JAN-2003.
PA   (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

  Query Match
  Best Local Similarity 26.6%; Score 144; DB 7; Length 367;
  Pred. No. 0.0014;
RESULT 1184

ID   ADE08316 standard; protein; 538 AA.
DE   Novel protein (useful for identifying genetic disorders) #471.
PN   WO2003054152-A2.
PD   03-JUL-2003.
PA   (PEKE) PE CORP NY.

  Query Match
  Best Local Similarity 26.6%; Score 144; DB 7; Length 538;
  Pred. No. 0.0024;
RESULT 1185

ID   ABB63044 standard; protein; 467 AA.
DE   Drosophila melanogaster polypeptide SEQ ID NO 15924.
PN   WO200171042-A2.
PD   27-SEP-2001.
PA   (PEKE) PE CORP NY.

  Query Match
  Best Local Similarity 20.7%; Score 143.5; DB 4; Length 467;
  Pred. No. 0.0022;
RESULT 1186

ID   ADG97401 standard; protein; 396 AA.
DE   Murine nectin-like protein 1.
PN   WO2003064992-A2.
PD   07-AUG-2003.
PA   (PLAN-) PLANET BIOTECHNOLOGY INC.
PA   (LARR/) LARRICK J W.
PA   (WYCO/) WYCOFF K L.

  Query Match
  Best Local Similarity 22.1%; Score 143; DB 7; Length 396;
  Pred. No. 0.0021;
RESULT 1187

ID   AAY69287 standard; protein; 398 AA.
DE   Amino acid sequence of long extracellular form of murine B7-1 (CD80).
PN   WO200008057-A2.
PD   17-FEB-2000.
PA   (IMMV) IMMUNEX CORP.

  Query Match
  Best Local Similarity 19.6%; Score 142.5; DB 3; Length 398;
  Pred. No. 0.0021;
RESULT 1188

ID   AAB00868 standard; protein; 404 AA.
DE   Mouse brain immunoglobulin superfamily receptor (BigR) protein.
PN   WO200129083-A1.
PD   26-APR-2001.
PA   (TEXA-) TEXAS BIOTECHNOLOGY CORP.

  Query Match
  Best Local Similarity 19.6%; Score 142.5; DB 4; Length 404;
  Pred. No. 0.0022;
RESULT 1189

ID ADJ70907 standard; protein; 450 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2713.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
PN Query Match   6.8%;   Score 142; DB 7; Length 450;
RESULT 1190
    Best Local Similarity   23.0%;   Pred. No. 0.0028;
ID ABP70430 standard; protein; 305 AA.
DE Amino acid sequence of murine TIM-1 BALB/c allele.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
PN Query Match   6.7%;   Score 141.5; DB 6; Length 305;
RESULT 1191
    Best Local Similarity   24.7%;   Pred. No. 0.0018;
ID ADE08000 standard; protein; 376 AA.
DE Novel protein (useful for identifying genetic disorders) #155.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
PN Query Match   6.7%;   Score 141.5; DB 7; Length 376;
RESULT 1192
    Best Local Similarity   25.2%;   Pred. No. 0.0024;
ID ADO47897 standard; protein; 463 AA.
DE Mouse protein SEQ ID NO:14.
PN WO2004076572-A2.
PD 22-JAN-2004.
PA (NUVE-) NUVELO INC.
PN Query Match   6.7%;   Score 141.5; DB 8; Length 463;
RESULT 1193
    Best Local Similarity   21.1%;   Pred. No. 0.0032;
ID AB080469 standard; protein; 3475 AA.
DE Human cancer-associated protein HP13-036.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
PN Query Match   6.7%;   Score 141.5; DB 8; Length 3475;
RESULT 1194
    Best Local Similarity   27.5%;   Pred. No. 0.0032;
ID ABB71502 standard; protein; 1052 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41298.
PN WO2001171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
PN Query Match   6.7%;   Score 141; DB 4; Length 1052;
RESULT 1195
    Best Local Similarity   25.1%;   Pred. No. 0.011;
ID AAW69698 standard; protein; 352 AA.
DE Mouse coxsackievirus and Ad2 and Ad5 receptor MCAR protein.
PN WO9833819-A1.
PD 06-AUG-1998.
PA (UYNY) UNIV NEW YORK STATE.
PN Query Match   6.7%;   Score 140.5; DB 2; Length 352;
RESULT 1196
    Best Local Similarity   25.4%;   Pred. No. 0.0026;
ID ABB63920 standard; protein; 359 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18552.
PN WO2001171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
PN Query Match   6.7%;   Score 140.5; DB 4; Length 359;
RESULT 1197
    Best Local Similarity   23.0%;   Pred. No. 0.0027;
ID AAW57213 standard; protein; 376 AA.
DE Mouse coxsackievirus and adenovirus receptor.
PN WO9811221-A2.
PD 19-MAR-1998.
PA (DAND) DANA FARBER CANCER INST INC.
PN Query Match   6.7%;   Score 140.5; DB 2; Length 376;
RESULT 1198
    Best Local Similarity   25.4%;   Pred. No. 0.0029;

ID ADP56685 standard; protein; 265 AA.
DE Human junction adhesion molecule 3 splice variant 2 (huJAM3sv2) protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (EILI) LILLY & CO ELI.
PN Query Match   6.6%;   Score 139.5; DB 3; Length 265;
RESULT 1199
    Best Local Similarity   24.0%;   Pred. No. 0.0021;
ID AAY96294 standard; protein; 310 AA.
DE Human IGFAM-6 immunoglobulin.
PN WO2000029583-A2.
PD 25-MAY-2000.
PA (INCY-) INCYTE PHARM INC.
PN Query Match   6.6%;   Score 139.5; DB 8; Length 310;
RESULT 1200
    Best Local Similarity   22.0%;   Pred. No. 0.0027;
ID ADP56683 standard; protein; 310 AA.
DE Human junction adhesion molecule 3 (huJAM3) full-length protein.
PN WO2004053058-A2.
PD 24-JUN-2004.
PA (EILI) LILLY & CO ELI.
PN Query Match   6.6%;   Score 139.5; DB 8; Length 310;
RESULT 1201
    Best Local Similarity   22.0%;   Pred. No. 0.0027;
ID ADQ81888 standard; protein; 413 AA.
DE Novel human immunosupressive receptor MCD055 protein sequence SeqID2.
PN JP2004208583-A.
PD 29-JUL-2004.
PA (MOCH) MOCHIDA PHARM CO LTD.
PA (BIOT-) BIOTECHNOLOGY KAIHATSU GIJUTSU KENKYU KU.
PN Query Match   6.6%;   Score 139.5; DB 8; Length 413;
RESULT 1202
    Best Local Similarity   23.3%;   Pred. No. 0.004;
ID AAE23555 standard; protein; 370 AA.
DE Human FAIL protein #4.
PN EP1201681-A1.
PD 02-MAY-2002.
PA (MILL-) MILLENNIUM PHARM INC.
PN Query Match   6.6%;   Score 139; DB 5; Length 370;
RESULT 1203
    Best Local Similarity   25.3%;   Pred. No. 0.0038;
ID ABG72460 standard; protein; 561 AA.
DE Human platelet derived growth factor receptor beta truncation mutant.
PN US2002111304-A1.
PD 15-AUG-2002.
PA (KAZL/) KAZLAUSKAS A.
PA (IKUN/) IKUNO Y.
PN Query Match   6.6%;   Score 139; DB 6; Length 561;
RESULT 1204
    Best Local Similarity   19.7%;   Pred. No. 0.0069;
ID ABG20753 standard; protein; 1089 AA.
DE Novel human diagnostic protein #20744.
PN WO2001175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
PN Query Match   6.6%;   Score 139; DB 4; Length 1089;
RESULT 1205
    Best Local Similarity   19.7%;   Pred. No. 0.018;
ID ABG72455 standard; protein; 1090 AA.
DE Human platelet derived growth factor receptor beta.
PN US2002111304-A1.
PD 15-AUG-2002.
PA (KAZL/) KAZLAUSKAS A.
PA (IKUN/) IKUNO Y.
PN Query Match   6.6%;   Score 139; DB 6; Length 1090;
RESULT 1206
    Best Local Similarity   19.7%;   Pred. No. 0.018;
ID AAP90127 standard; protein; 1106 AA.
DE Platelet derived growth factor receptor.
PN EP325224-A.
PD 26-JUL-1989.
PA (ZYMO) ZYMOGENETICS INC.
PN Query Match   6.6%;   Score 139; DB 1; Length 1106;

Best Local Similarity   19.7%;   Pred. No. 0.018;

RESULT 1207
ID   AAR26205 standard; protein; 1106 AA.
DE   Type B human platelet-derived growth factor receptor.
PN   WO9213867-A1.
PD   20-AUG-1992.
PA   (CORT-) COR THERAPEUTICS INC.
Query Match
Best Local Similarity   19.7%;   Score 139;   DB 2;   Length 1106;
Best Local Similarity   19.7%;   Pred. No. 0.018;

RESULT 1208
ID   AAR99690 standard; protein; 1106 AA.
DE   Platelet-derived growth factor receptor.
PN   EP721983-A1.
PD   17-JUL-1996.
PA   (ZYMO-) ZYMOGENETICS INC.
Query Match
Best Local Similarity   19.7%;   Score 139;   DB 2;   Length 1106;
Best Local Similarity   19.7%;   Pred. No. 0.018;

RESULT 1209
ID   ABG72457 standard; protein; 1106 AA.
DE   Human platelet derived growth factor receptor beta mutant T672M.
PN   US2002111304-A1.
PD   15-AUG-2002.
PA   (KAZL/) KAZLAUSKAS A.
Query Match
Best Local Similarity   19.7%;   Score 139;   DB 6;   Length 1106;
Best Local Similarity   19.7%;   Pred. No. 0.018;

RESULT 1210
ID   ABG72456 standard; protein; 1106 AA.
DE   Human platelet derived growth factor receptor beta mutant E594K.
PN   US2002111304-A1.
PD   15-AUG-2002.
PA   (KAZL/) KAZLAUSKAS A.
Query Match
Best Local Similarity   19.7%;   Score 139;   DB 6;   Length 1106;
Best Local Similarity   19.7%;   Pred. No. 0.018;

RESULT 1211
ID   ABG72459 standard; protein; 1106 AA.
DE   Human platelet derived growth factor receptor beta mutant L867M.
PN   US2002111304-A1.
PD   15-AUG-2002.
PA   (KAZL/) KAZLAUSKAS A.
Query Match
Best Local Similarity   19.7%;   Score 139;   DB 6;   Length 1106;
Best Local Similarity   19.7%;   Pred. No. 0.018;

RESULT 1212
ID   ABG72458 standard; protein; 1106 AA.
DE   Human platelet derived growth factor receptor beta mutant D826N.
PN   US2002111304-A1.
PD   15-AUG-2002.
PA   (KAZL/) KAZLAUSKAS A.
Query Match
Best Local Similarity   19.7%;   Score 139;   DB 6;   Length 1106;
Best Local Similarity   19.7%;   Pred. No. 0.018;

RESULT 1213
ID   ABP96311 standard; protein; 1106 AA.
DE   Human platelet-derived growth factor receptor beta protein.
PN   WO2003016540-A2.
PD   27-FEB-2003.
PA   (UYYO-) UNIV YORK.
Query Match
Best Local Similarity   19.7%;   Score 139;   DB 7;   Length 1106;
Best Local Similarity   19.7%;   Pred. No. 0.018;

RESULT 1214
ID   ABR84719 standard; protein; 1106 AA.
DE   Human PDGF beta receptor protein.
PN   WO2003070083-A2.
PD   28-AUG-2003.
PA   (CORR-) CORNELL RES FOUND INC.
     (EDEL/) EDELBERG J M.
     (RAFI/) RAFII S.
     (HONG/) HONG M K.
     (LANZ/) LANZA R P.
     (WEST/) WEST M D.
Query Match
Best Local Similarity   19.7%;   Score 139;   DB 7;   Length 1106;
Best Local Similarity   19.7%;   Pred. No. 0.018;

RESULT 1215
ID   ADF45082 standard; protein; 1106 AA.
DE   Human kinase PDGFR-b.
PN   WO2003081210-A2.
PD   02-OCT-2003.
PA   (SUNE-) SUNESIS PHARM INC.
Query Match
Best Local Similarity   19.7%;   Score 139;   DB 7;   Length 1106;
Best Local Similarity   19.7%;   Pred. No. 0.018;

RESULT 1216
ID   ABO84679 standard; protein; 1106 AA.
DE   Human cancer-associated protein HP20-018.3.
PN   WO2004074320-A2.
PD   02-SEP-2004.
PA   (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity   19.7%;   Score 139;   DB 8;   Length 1106;
Best Local Similarity   19.7%;   Pred. No. 0.018;

RESULT 1217
ID   AAY96735 standard; protein; 310 AA.
DE   PRO1868, an A33 antigen homologue.
PN   WO2000036102-A2.
PD   22-JUN-2000.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   21.8%;   Score 138.5;   DB 3;   Length 310;
Best Local Similarity   21.8%;   Pred. No. 0.0033;

RESULT 1218
ID   AAB33457 standard; protein; 310 AA.
DE   Human PRO1868 protein UNQ859 SEQ ID NO:193.
PN   WO2000053758-A2.
PD   14-SEP-2000.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   21.8%;   Score 138.5;   DB 3;   Length 310;
Best Local Similarity   21.8%;   Pred. No. 0.0033;

RESULT 1219
ID   AAB27276 standard; protein; 310 AA.
DE   Human confluency regulated adhesion molecule 1 #2.
PN   WO2000053749-A2.
PD   14-SEP-2000.
PA   (RMFD-) RMF DICTAGENE SA.
Query Match
Best Local Similarity   21.8%;   Score 138.5;   DB 3;   Length 310;
Best Local Similarity   21.8%;   Pred. No. 0.0033;

RESULT 1220
ID   AAB80272 standard; protein; 310 AA.
DE   Human PRO1868 protein.
PN   WO2001043111-A1.
PD   18-JAN-2001.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   21.8%;   Score 138.5;   DB 3;   Length 310;
Best Local Similarity   21.8%;   Pred. No. 0.0033;

RESULT 1221
ID   AAM93905 standard; protein; 310 AA.
DE   Human polypeptide, SEQ ID NO: 4051.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
Query Match
Best Local Similarity   21.8%;   Score 138.5;   DB 4;   Length 310;
Best Local Similarity   21.8%;   Pred. No. 0.0033;

RESULT 1222
ID   AAM93323 standard; protein; 310 AA.
DE   Human polypeptide, SEQ ID NO: 2845.
PN   EP1130094-A2.
PD   05-SEP-2001.
PA   (HELI-) HELIX RES INST.
Query Match
Best Local Similarity   21.8%;   Score 138.5;   DB 4;   Length 310;
Best Local Similarity   21.8%;   Pred. No. 0.0033;

RESULT 1223
ID   AAU12440 standard; protein; 310 AA.
DE   Human PRO1868 polypeptide sequence.
PN   WO2001040466-A2.
PD   07-JUN-2001.
PA   (GETH) GENENTECH INC.
Query Match
Best Local Similarity   21.8%;   Score 138.5;   DB 4;   Length 310;

RESULT 1224
ID   AAB80383 standard; protein; 310 AA.
DE   Secreted protein encoded by gene #13.
PN   WO200107459-A1.
PD   01-FEB-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   21.8%; Score 138.5; DB 4; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1225
ID   AAB80408 standard; protein; 310 AA.
DE   Secreted protein encoded by gene #38.
PN   WO200107459-A1.
PD   01-FEB-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   21.8%; Score 138.5; DB 4; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1226
ID   AAB80409 standard; protein; 310 AA.
DE   Secreted protein encoded by gene #39.
PN   WO200107459-A1.
PD   01-FEB-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   21.8%; Score 138.5; DB 4; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1227
ID   ABG92709 standard; protein; 310 AA.
DE   Human secreted protein PRO1868.
PN   US2002098506-A1.
PD   25-JUL-2002.
PA   (GETH) GENENTECH INC.
Query Match   21.8%; Score 138.5; DB 5; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1228
ID   ABG91361 standard; protein; 310 AA.
DE   Novel human secreted protein #7.
PN   US2002098505-A1.
PD   25-JUL-2002.
PA   (GETH) GENENTECH INC.
Query Match   21.8%; Score 138.5; DB 5; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1229
ID   ABB84947 standard; protein; 310 AA.
DE   Human PRO1868 protein sequence SEQ ID NO:262.
PN   WO200200690-A2.
PD   03-JAN-2002.
PA   (GETH) GENENTECH INC.
Query Match   21.8%; Score 138.5; DB 5; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1230
ID   ABG65297 standard; protein; 310 AA.
DE   Human albumin fusion protein #1972.
PN   WO200177137-A1.
PD   18-OCT-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   21.8%; Score 138.5; DB 5; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1231
ID   ABG65296 standard; protein; 310 AA.
DE   Human albumin fusion protein #1971.
PN   WO200177137-A1.
PD   18-OCT-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   21.8%; Score 138.5; DB 5; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1232
ID   ABG65298 standard; protein; 310 AA.
DE   Human albumin fusion protein #1973.
PN   WO200177137-A1.
PD   18-OCT-2001.
PA   (HUMA-) HUMAN GENOME SCI INC.
Query Match   21.8%; Score 138.5; DB 5; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1233
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ID   ABG31401 standard; protein; 310 AA.
DE   Human PRO1868 polypeptide.
PN   US2002098507-A1.
PD   25-JUL-2002.
PA   (GETH) GENENTECH INC.
Query Match   21.8%; Score 138.5; DB 5; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1234
ID   ABB95553 standard; protein; 310 AA.
DE   Human angiogenesis related protein PRO1868 SEQ ID NO: 262.
PN   WO200208284-A2.
PD   31-JAN-2002.
PA   (GETH) GENENTECH INC.
Query Match   21.8%; Score 138.5; DB 6; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1235
ID   ABU71650 standard; protein; 310 AA.
DE   Human PRO polypeptide #61.
PN   US2002146709-A1.
PD   10-OCT-2002.
PA   (GETH) GENENTECH INC.
PA   (BAKE/) BAKER K P.
PA   (FERR/) FERRARA N.
PA   (GERB/) GERBER H.
PA   (GERR/) GERRITSEN M E.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (HILL/) HILLAN K J.
PA   (MARS/) MARSTERS S A.
PA   (PAN J/) PAN J.
PA   (PAON/) PAONI N F.
PA   (STEP/) STEPHAN J F.
PA   (WATA/) WATANABE C K.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
Query Match   21.8%; Score 138.5; DB 6; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1236
ID   ABU72377 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2002182618-A1.
PD   05-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match   21.8%; Score 138.5; DB 6; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1237
ID   ABU80867 standard; protein; 310 AA.
DE   Human secreted and transmembrane polypeptide PRO1868.
PN   US2002192668-A1.
PD   19-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match   21.8%; Score 138.5; DB 6; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1238
ID   ABO17884 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003032156-A1.
PD   13-FEB-2003.
PA   (GETH) GENENTECH INC.
Query Match   21.8%; Score 138.5; DB 6; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1239
ID   ABU71505 standard; protein; 310 AA.
DE   Human PRO polypeptide.
PN   US2003192659-A1.
PD   19-DEC-2002.
PA   (GETH) GENENTECH INC.
Query Match   21.8%; Score 138.5; DB 6; Length 310;
Best Local Similarity 6.6%; Pred. No. 0.0033;

RESULT 1240
ID   ADA57610 standard; protein; 310 AA.
DE   Human secreted protein #592.

PN WO200210299-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1241
ID ADA57611 standard; protein; 310 AA.
DE Human secreted protein #592.
PN WO200210299-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1242
ID ADA57309 standard; protein; 310 AA.
DE Human secreted protein #592.
PN WO200210299-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1243
ID ABP71277 standard; protein; 310 AA.
DE Human junctional adhesion molecule 3 (JAM3).
PN WO200306673-A2.
PD 23-JAN-2003;
PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1244
ID ABU81138 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003004311-A1.
PD 02-JAN-2003;
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1245
ID ABU71951 standard; protein; 310 AA.
DE Human secreted/transmembrane protein PRO1868.
PN US2003003530-A1.
PD 02-JAN-2003;
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1246
ID ABO01834 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1247
ID ABU66838 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1248
ID ABU5407 standard; protein; 310 AA.
DE Human secreted/transmembrane protein.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1249
ID AB047422 standard; protein; 310 AA.
DE Human secreted/transmembrane polypeptide PRO1868.
PN US2003044839-A1.

PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1250
ID ABG73314 standard; protein; 310 AA.
DE Human PRO1868 polypeptide.
PN US2002164646-A1.
PD 07-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1251
ID ABU59919 standard; protein; 310 AA.
DE Novel secreted and transmembrane protein PRO1868.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1252
ID ABO25109 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #63.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1253
ID ABU64559 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, (PRO) #269.
PN US2003036374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1254
ID ABO17405 standard; protein; 310 AA.
DE Human secreted protein PRO1868.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1255
ID ABO14925 standard; protein; 310 AA.
DE Human secreted / transmembrane polypeptide PRO1868.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1256
ID ABU60813 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #7.
PN US2002160392-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1257
ID ABU67114 standard; protein; 310 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 538.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 6; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1258
ID ABU81236 standard; protein; 310 AA.
DE Human PRO1917 polypeptide.
PN US2003032060-A1.
PD 13-FEB-2003.

RESULT 1259
ID   ABU69682 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868+H30.
PN   US20030017463-A1
PD   23-JAN-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1260
ID   ABO14864 standard; protein; 310 AA.
DE   Human secreted / transmembrane polypeptide PRO1868.
PN   US20030027143-A1
PD   06-FEB-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1261
ID   ADA46057 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030022328-A1
PD   30-JAN-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1262
ID   ADA76488 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030073212-A1
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1263
ID   ADB29627 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US20030092002-A1
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1264
ID   ADA19138 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030054517-A1
PD   20-MAR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1265
ID   ADA61761 standard; protein; 310 AA.
DE   Homo sapiens.
PN   US20030049816-A1
PD   13-MAR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1266
ID   ADB19546 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030068796-A1
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1267
ID   ADB28087 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030082704-A1
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1268
ID   ADA86566 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030082711-A1
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1269
ID   ADB16130 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030087350-A1
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1270
ID   ADA47916 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030073215-A1
PD   17-APR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1271
ID   ADA18484 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US20030039971-A1
PD   27-FEB-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1272
ID   ABO32816 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein PRO1868.
PN   US20030045693-A1
PD   06-MAR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1273
ID   ADA67711 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030068795-A1
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1274
ID   ADB30718 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030068794-A1
PD   10-APR-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1275
ID   ADA86014 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030082693-A1
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%; Pred. No. 0.0033;

RESULT 1276
ID   ADA97226 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030082705-A1
PD   01-MAY-2003.
PA   (GETH) GENENTECH INC.
Best Local Similarity 21.8%; Score 138.5; DB 6; Length 310;
Query Match 6.6%;

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Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1277
ID   ADA79530 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030082763-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1278
ID   ADA87669 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030087345-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1279
ID   ADB16871 standard; protein; 310 AA.
DE   Human PRO polypeptide #61.
PN   US20030087349-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1280
ID   ABO34876 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030044793-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1281
ID   ADA16459 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US20030049621-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1282
ID   ADA91963 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030082694-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1283
ID   ADB15026 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030087351-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1284
ID   ADB18987 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030073211-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1285
ID   ADA94202 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030077722-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;


RESULT 1286
ID   ADB20098 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030082691-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1287
ID   ADB13410 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030082710-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1288
ID   ABO43417 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030044945-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1289
ID   ADA74664 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030068798-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1290
ID   ADA42604 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US20030054401-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1291
ID   ADB24897 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 538.
PN   US20030077713-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1292
ID   ADA82421 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030082701-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1293
ID   ADA75384 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US20030073216-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;   Pred. No. 0.0033;
RESULT 1294
ID   ADA85462 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030082695-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match      6.6%;   Score 138.5;   DB 6;   Length 310;
     Best Local Similarity   21.8%;
RESULT 1295
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ID   ADA84910 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003082708-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1296
ID   ABO17554 standard; protein; 310 AA.
DE   Human PRO polypeptide #61.
PN   US2003064367-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1297
ID   ADB30166 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003073214-A1.
PD   17-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1298
ID   ADA80694 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003082761-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1299
ID   ADA75936 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003082703-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1300
ID   ADA47161 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003073210-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1301
ID   ADB25457 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003077715-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1302
ID   ADB93633 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003092147-A1.
PD   15-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1303
ID   ADB26983 standard; protein; 310 AA.

RESULT 1304
ID   ADB31270 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003096386-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1305
ID   ABU62957 standard; protein; 310 AA.
DE   Human PRO1868 protein.
PN   US2003054447-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1306
ID   ADA61198 standard; protein; 310 AA.
DE   Homo sapiens.
PN   US2003049817-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1307
ID   ADB24345 standard; protein; 310 AA.
DE   Human PRO polypeptide SEQ ID NO 538.
PN   US2003077714-A1.
PD   24-APR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1308
ID   ADA96674 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003082690-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1309
ID   ADA81246 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003082702-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1310
ID   ADA96122 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003082759-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1311
ID   ADB26431 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003082760-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1312
ID   ADB21916 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003082765-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match 6.6%;
     Best Local Similarity 21.8%;
     Score 138.5; DB 6; Length 310;

RESULT 1313
ID   ADA77695 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
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PN US200306879?-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
RESULT 1314
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADB18435 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
RESULT 1315
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADA87118 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 1316
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADA16883 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
RESULT 1317
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADA13312 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
RESULT 1318
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADA42180 standard; protein; 310 AA.
DE Human secreted and transmembrane protein PRO1868.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 1319
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADA88221 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 1320
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADA46609 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
RESULT 1321
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADA17527 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
RESULT 1322
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADA43030 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054351-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
RESULT 1323
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADB28639 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 1324
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADB29191 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 1325
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID AB001894 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003027256-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
RESULT 1326
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADA77143 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
RESULT 1327
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADA88773 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
RESULT 1328
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADA97778 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 1329
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADB27535 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
RESULT 1330
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID ADB22468 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
RESULT 1331
Query Match
Best Local Similarity 21.8%; Score 138.5; DB 7; Length 310;
ID AB017615 standard; protein; 310 AA.
DE Human PRO polypeptide #61.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match

Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1332
ID ADA67159 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1333
ID ADB23020 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1334
ID ADB23793 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1335
ID ADA92515 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1336
ID ADB15578 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1337
ID ADB38830 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1338
ID ADB38278 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1339
ID ADB66750 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1340
ID ADB89830 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1341
ID ADB90562 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1342
ID ADB77948 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1343
ID ADB39663 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein, #65.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1344
ID ADB75084 standard; protein; 310 AA.
DE Novel human secreted/transmembrane protein, #65.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1345
ID ADB47286 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1346
ID ADB86893 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1347
ID ADB77498 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1348
ID ADB34655 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1349
ID ADB35759 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;
RESULT 1350

ID ADB34103 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1351
ID ADB35207 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1352
ID ADB36311 standard; protein; 310 AA.
DE Human PRO polypeptide SEQ ID NO 538.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1353
ID ADB46706 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1354
ID ADC28731 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1355
ID ADC39931 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1356
ID ADC40445 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1357
ID ADC19269 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1358
ID ADC34569 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1359
ID ADC29624 standard; protein; 310 AA.

DE Human secreted/transmembrane protein, #65.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1360
ID ADC29155 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1361
ID ADC41040 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1362
ID ADC19697 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1363
ID ADC34145 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1364
ID ADC13215 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1365
ID AAB38826 standard; protein; 310 AA.
DE Human PRO1868 protein.
PN US2003077657-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1366
ID ADC50579 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1367
ID ADC72126 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1368
ID ADC60105 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.

PN US20030092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1369
ID ADC53112 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US20030087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1370
ID ADC57466 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US20030087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1371
ID ADC60657 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US20030087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1372
ID ADC51132 stahdard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US20030087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1373
ID ADC65659 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1374
ID ADC54757 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US20030087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1375
ID ADC53718 stahdard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US20030087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1376
ID ADC59241 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US20030087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1377
ID ADC56619 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US20030087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1378
ID ADC58689 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein Seq ID538.
PN US20030087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1379
ID ADC12667 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US20030082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1380
ID ADC74383 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1016.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1381
ID ADC74606 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1239.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1382
ID ADC74607 standard; protein; 310 AA.
DE Human secreted protein - SEQ ID 1240.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1383
ID ADD03363 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US20030092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1384
ID ADC90355 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US20030087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1385
ID ADC69774 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1386
ID ADC48663 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030194773-A1.
PD 16-OCT-2003.

Left column

RESULT 1387
ID   ADD10192 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194776-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1388
ID   ADD04767 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein #269.
PN   US2003087354-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1389
ID   ADD80723 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003092103-A1.
PD   15-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1390
ID   ADD11230 standard; protein; 310 AA.
DE   Human secreted and transmembrane protein PRO1868.
PN   US2003194774-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1391
ID   ADD10551 standard; protein; 310 AA.
DE   Human secreted/transmembrane PRO polypeptide #131.
PN   US2003105011-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1392
ID   ADC48111 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194771-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1393
ID   ADD05222 standard; protein; 310 AA.
DE   Human secreted and transmembrane protein, #65.
PN   US2003104469-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1394
ID   ADC80171 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane PRO polypeptide #131.
PN   US2003087358-A1.
PD   08-MAY-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1395
ID   ADD11511 standard; protein; 310 AA.
DE   Human secreted/transmembrane PRO polypeptide #131.
PN   US2003105013-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

Right column

RESULT 1396
ID   ADD09640 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194775-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1397
ID   ADD04228 standard; protein; 310 AA.
DE   Human secreted and transmembrane protein, #65.
PN   US2003104381-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1398
ID   ADD03804 standard; protein; 310 AA.
DE   Human secreted and transmembrane protein, #65.
PN   US2003108983-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1399
ID   ADD41353 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003108438-A1.
PD   12-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1400
ID   ADD52492 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003203438-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1401
ID   ADD53232 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194769-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1402
ID   ADD53784 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003203437-A1.
PD   30-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1403
ID   ADD37304 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane PRO polypeptide #131.
PN   US2003105012-A1.
PD   05-JUN-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1404
ID   ADD51940 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003194779-A1.
PD   16-OCT-2003.
PA   (GETH) GENENTECH INC.
Query Match   6.6%; Score 138.5; DB 7; Length 310;

Best Local Similarity   21.8%;   Pred. No. 0.0033;

RESULT 1405
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (GETH) GENENTECH INC.
PD   30-OCT-2003.
PN   US2003203431-A1.
DE   Human PRO polypeptide #269.
ID   ADD02739 standard; protein; 310 AA.

RESULT 1406
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (HUMA-) HUMAN GENOME SCI INC.
PD   14-NOV-2002.
PN   WO200290526-A2.
DE   Human secreted protein #289.
ID   ADD38106 standard; protein; 310 AA.

RESULT 1407
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (HUMA-) HUMAN GENOME SCI INC.
PD   14-NOV-2002.
PN   WO200290526-A2.
DE   Human secreted protein #192.
ID   ADD38009 standard; protein; 310 AA.

RESULT 1408
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (HUMA-) HUMAN GENOME SCI INC.
PD   14-NOV-2002.
PN   WO200290526-A2.
DE   Human secreted protein #288.
ID   ADD38105 standard; protein; 310 AA.

RESULT 1409
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (GETH) GENENTECH INC.
PD   30-OCT-2003.
PN   US2003203430-A1.
DE   Novel human secreted and transmembrane protein PRO1868.
ID   ADD54355 standard; protein; 310 AA.

RESULT 1410
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (GETH) GENENTECH INC.
PD   30-OCT-2003.
PN   US2003203432-A1.
DE   Human PRO polypeptide #269.
ID   ADD02173 standard; protein; 310 AA.

RESULT 1411
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (GETH) GENENTECH INC.
PD   23-OCT-2003.
PN   US2003199030-A1.
DE   Human PRO polypeptide #269.
ID   ADD92672 standard; protein; 310 AA.

RESULT 1412
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (GETH) GENENTECH INC.
PD   23-OCT-2003.
PN   US2003199055-A1.
DE   Human PRO polypeptide #269.
ID   ADD91568 standard; protein; 310 AA.

RESULT 1413
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (GETH) GENENTECH INC.
PD   23-OCT-2003.
PN   US2003199057-A1.
DE   Human PRO polypeptide #269.
ID   ADE04182 standard; protein; 310 AA.

RESULT 1414
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (GETH) GENENTECH INC.
PD   16-OCT-2003.
PN   US2003194765-A1.
DE   Novel human secreted and transmembrane protein PRO1868.
ID   ADB32479 standard; protein; 310 AA.

RESULT 1415
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (GETH) GENENTECH INC.
PD   23-OCT-2003.
PN   US2003199056-A1.
DE   Human PRO polypeptide #269.
ID   ADB22411 standard; protein; 310 AA.

RESULT 1416
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (GETH) GENENTECH INC.
PD   30-OCT-2003.
PN   US2003203428-A1.
DE   Human PRO polypeptide #269.
ID   ADD79635 standard; protein; 310 AA.

RESULT 1417
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (GETH) GENENTECH INC.
PD   16-OCT-2003.
PN   US2003194772-A1.
DE   Human PRO polypeptide #269.
ID   ADB42171 standard; protein; 310 AA.

RESULT 1418
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (GETH) GENENTECH INC.
PD   23-OCT-2003.
PN   US2003199023-A1.
DE   Human PRO polypeptide #269.
ID   ADB17988 standard; protein; 310 AA.

RESULT 1419
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (GETH) GENENTECH INC.
PD   16-OCT-2003.
PN   US2003194767-A1.
DE   Human PRO polypeptide #269.
ID   ADD92120 standard; protein; 310 AA.

RESULT 1420
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (GETH) GENENTECH INC.
PD   23-OCT-2003.
PN   US2003199053-A1.
DE   Novel human secreted and transmembrane protein PRO1868.
ID   ADD33583 standard; protein; 310 AA.

RESULT 1421
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (GETH) GENENTECH INC.
PD   16-OCT-2003.
PN   US2003194791-A1.
DE   Novel human secreted and transmembrane protein PRO1868.
ID   ADB34135 standard; protein; 310 AA.

RESULT 1422
Best Local Similarity   21.8%;   Score 138.5;   DB 7;   Length 310;
Query Match   6.6%;   Pred. No. 0.0033;
PA   (GETH) GENENTECH INC.
PD   06-NOV-2003.
PN   US2003207417-A1.
DE   Human PRO polypeptide #269.
ID   ADD80187 standard; protein; 310 AA.

RESULT 1423

ID ADD93224 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1424
ID ADE19644 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1425
ID ADE35056 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1426
ID ADE19092 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1427
ID ADE43288 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1428
ID ADD96077 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1429
ID ADE22963 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1430
ID ADD79081 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1431
ID ADE33031 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1432
ID ADE42723 standard; protein; 310 AA.

DE Human PRO polypeptide #269.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1433
ID ADD80739 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1434
ID ADB89767 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1435
ID ADE41051 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1436
ID ADE04850 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1437
ID ADB92979 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1438
ID ADG21688 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1439
ID ADG23329 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1440
ID ADF97664 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%;
Best Local Similarity 21.8%;
Score 138.5; DB 7; Length 310;

RESULT 1441
ID ADG80728 standard; protein; 310 AA.
DE Human PRO polypeptide #269.

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PN   US20032073?3-A1
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
ID   ADG80176 standard; protein; 310 AA.
RESULT 1442
DE   Human PRO polypeptide #269.
PN   US20032073?2-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
ID   ADH62558 standard; protein; 310 AA.
RESULT 1443
DE   Human PRO1868 protein.
PN   US200317156?-A1.
PD   11-SEP-2003.
PA   (ASHK/) ASHKENAZI A.
PA   (FONG/) FONG S.
PA   (GODD/) GODDARD A.
PA   (GURN/) GURNEY A L.
PA   (NAPI/) NAPIER M A.
PA   (TUMA/) TUMA? D.
PA   (WOOD/) WOOD W I.
PN   US20030399?2-A1.
PD   27-FEB-2003.
DE   Human secreted/transmembrane protein, #65.
ID   ADH59539 standard; protein; 310 AA.
RESULT 1444
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
PA   (GETH ) GENENTECH INC.
PD   06-NOV-2003.
PN   US20032073?9-A1.
DE   Novel human secreted and transmembrane protein PRO1868.
ID   ADH55468 standard; protein; 310 AA.
RESULT 1445
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
PA   (GETH ) GENENTECH INC.
PD   06-NOV-2003.
PN   US20032073?1-A1.
DE   Novel human secreted and transmembrane protein PRO1868.
ID   ADH56020 standard; protein; 310 AA.
RESULT 1446
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
PA   (GETH ) GENENTECH INC.
PD   06-NOV-2003.
PN   US20032073?9-A1.
DE   Human secreted/transmembrane protein, #65.
ID   ADI38318 standard; protein; 310 AA.
RESULT 1447
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
PA   (GETH ) GENENTECH INC.
PD   06-NOV-2003.
PN   US20030543?2-A1.
DE   Novel human secreted and transmembrane protein, #65.
ID   ADI64239 standard; protein; 310 AA.
RESULT 1448
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
PA   (GETH ) GENENTECH INC.
PD   20-MAR-2003.
PN   US20032073?5-A1.
DE   Novel human secreted and transmembrane protein PRO1868.
ID   ADI65188 standard; protein; 310 AA.
RESULT 1449
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
PA   (GETH ) GENENTECH INC.
PD   06-NOV-2003.
PN   US20032073?6-A1.
DE   Novel human secreted and transmembrane protein PRO1868.
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     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
ID   ADL63687 standard; protein; 310 AA.
RESULT 1450
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20032073?7-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
ID   ADH81549 standard; protein; 310 AA.
RESULT 1451
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20032073?7-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
ID   ADH82101 standard; protein; 310 AA.
RESULT 1452
DE   Human PRO1868 protein.
PN   US200317086?-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
ID   ADJ58818 standard; protein; 310 AA.
RESULT 1453
DE   Human PRO1868 protein.
PN   US200317086?-A1.
PD   11-SEP-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
ID   ADJ26586 standard; protein; 310 AA.
RESULT 1454
DE   Novel human secreted/transmembrane protein, #65.
PN   US200305434?-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
ID   ADM82718 standard; protein; 310 AA.
RESULT 1455
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030873?5-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
ID   ADN16117 standard; protein; 310 AA.
RESULT 1456
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030873?3-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
ID   ADN16746 standard; protein; 310 AA.
RESULT 1457
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030873?5-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
ID   ADN15565 standard; protein; 310 AA.
RESULT 1458
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US20030873?6-A1.
PD   08-MAY-2003.
PA   (GETH ) GENENTECH INC.
     Query Match    6.6%;  Score 138.5;  DB 7;  Length 310;
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Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1459
ID ADN15013 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US20030087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 7; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1460
ID ADC81275 standard; protein; 310 AA.
DE Novel human secreted and transmembrane protein PRO1868.
PN US20030092115-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1461
ID ADE79501 standard; protein; 310 AA.
DE Human secreted and transmembrane protein, #65.
PN US20030135025-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1462
ID ADD76723 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030100087-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1463
ID ADD88087 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1464
ID ADD86491 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1465
ID ADE79925 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US20030130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1466
ID ADE75939 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1467
ID ADE73601 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US20030129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1468
ID ADB41512 standard; protein; 310 AA.
DE Human secreted/transmembrane PRO polypeptide #131.
PN US20030100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1469
ID ADB23515 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1470
ID ADE24067 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1471
ID ADE24710 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1472
ID ADB87535 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1473
ID ADB89401 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1474
ID ADE74136 standard; protein; 310 AA.
DE Human secreted/transmembrane protein, #65.
PN US20030148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1475
ID ADE18540 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1476
ID ADB88849 standard; protein; 310 AA.
DE Human PRO polypeptide #269.
PN US20030199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 6.6%; Score 138.5; DB 8; Length 310;
Best Local Similarity 21.8%; Pred. No. 0.0033;

RESULT 1477

ID   ADE99690 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003211576-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1478
ID   ADE94869 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003211568-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1479
ID   ADE91280 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003199061-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1480
ID   ADE95421 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003199052-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1481
ID   ADE93531 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003199060-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1482
ID   ADF35112 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003199029-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1483
ID   ADE98809 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003211569-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1484
ID   ADE92427 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003199051-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1485
ID   ADE90728 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003199063-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1486
ID   ADE91875 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003199058-A1.
PD   23-OCT-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1487
ID   ADE99236 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003211568-A1.
PD   13-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1488
ID   ADG40706 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003225253-A1.
PD   04-DEC-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1489
ID   ADF74100 standard; protein; 310 AA.
DE   Human secreted/transmembrane protein, #65.
PN   US2003180312-A1.
PD   25-SEP-2003.
PA   (WILL/) WILLIAMS P M.
PA   (MATH/) MATHER J P.
PA   (GURN/) GURNEY A L.
PA   (GODO/) GODOWSKI P J.
PA   (GODD/) GODDARD A.
PA   (DESN/) DESNOYERS L.
PA   (WOOD/) WOOD W I.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1490
ID   ADG02454 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207352-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1491
ID   ADG22240 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207360-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1492
ID   ADG20310 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207376-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1493
ID   ADF98216 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207422-A1.
PD   06-NOV-2003.
PA   (GETH) GENENTECH INC.
     Query Match   6.6%;
     Best Local Similarity   21.8%;
     Score 138.5; DB 8; Length 310;

RESULT 1494
ID   ADG24433 standard; protein; 310 AA.
DE   Novel human secreted and transmembrane protein PRO1868.
PN   US2003207426-A1.
PD   06-NOV-2003.

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PA   (GETH ) GENENTECH INC.
     Query Match         6.6%;  Score 138.5;  DB 8;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
RESULT 1495
ID   ADF98787 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003208055-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         6.6%;  Score 138.5;  DB 8;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
RESULT 1496
ID   ADG03618 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207351-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         6.6%;  Score 138.5;  DB 8;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
RESULT 1497
ID   ADF99339 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207353-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         6.6%;  Score 138.5;  DB 8;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
RESULT 1498
ID   ADG16924 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207359-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         6.6%;  Score 138.5;  DB 8;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
RESULT 1499
ID   ADG05383 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207375-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         6.6%;  Score 138.5;  DB 8;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
RESULT 1500
ID   ADG19650 standard; protein; 310 AA.
DE   Human PRO polypeptide #269.
PN   US2003207425-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
     Query Match         6.6%;  Score 138.5;  DB 8;  Length 310;
     Best Local Similarity   21.8%;  Pred. No. 0.0033;
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